Title: Perfect score: Sequence:

US-10-018-924-2_COPY_22_146

8

protein

protein search, using sw model

GenCore version Copyright (c) 1993 - 2002

1 5.1.3 Compugen

October 17, 2002, 15:20:12;

Scoring table:

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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                                                                                                 ; MOLECULE TYPE: US-08-233-389C-1
                                                                                                             TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
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US-08-233-389C-1
                                                     Matches
                                                               Query Match
Best Local (
                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TETLEPHONE: (212) 596-9000
TETLEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1,
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE ~ ~ ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KITAMÜRA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 125
CITY: New Y
STATE: NY
COUNTRY: US
ZIP: 10020
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OPERATING SYSTEM: PC-DOS/MS-DOS
al Similarity
125; Conserv
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1251 Avenue of the Americas
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US-08-941-262-1
US-08-941-262-3
US-08-453-956-15
US-08-452-930-15
PCT-US93-08174-15
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US-09-18-6278-10
                                              Score 655; DB 1
Pred. No. 1e-72;
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Result No.

Query Match

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SUMMARIES

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US-08-233-389C-1
US-08-486-596A-1
US-08-486-596A-3
US-08-001-863-1
US-08-801-863-3
US-08-801-863-3
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US-09-286-529-2

Database

Issued_Patents_AA:*

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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231628

231628 segs, 24425594 residues

Searched:

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RESULT 3
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KITAMURA, Kazuo APPLICANT: KANGAWA, Kenji APPLICANT: MATSUO, Hisayuki APPLICANT: ETO, Tanenao TITLE OF INVENTION: ADRENOMED NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 596-9090 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 SPQGY 146
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: CONCUCASSIFICATION: 53
                                                                                                                              121 SPQGY 125
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                                                                                                                                                        22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 81
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
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amino acid
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100.0%; Pred. No. 1e-72;
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                 Sequence 1, Application US/09004713
Patent No. 5910416
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 596-90
TELEFAX: (212) 596-90
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY_AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KITAMURA,
APPLICANT: KANGAWA,
APPLICANT: MATSUO, H
APPLICANT: ETO, Tane
APPLICANT: ETO, Tane
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acid
                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                               STREET: LAU-
STREET: New York
CITY: New York
CTATE: NY
                                                                                               TITLE OF INVENTION: ADRENOMEDULLIN NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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ZIP: 10020
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COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                      142 SPQGY 146
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                                                                                    ADDRESSEE:
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KANGAWA, Kenji
MATSUO, Hisayuki
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                                                                        E: c/o FISH & NEAVE
1251 Avenue of the Americas
                              USA
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MATSUO, Hisayuki
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100.0%; Pred. No. 1
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-801-863-3
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            Matches 114;
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-233-389C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08801863 Patent No. 5830703
                                                                                                                                        TELEFAX: (212) 596-9090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, ve CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 596-9090 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1251 AV
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 ASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
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                                                                                                                                                                                                                                                                                                                                                                                                           10020
                                                                                                            : 188 amino acids
amino acid
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amino acid
OGY: linear
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanenao
                     93.3%;
91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.3%;
    Score 611; DB 2; I
Pred. No. 2.6e-67;
8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 611; DB 1;
Pred. No. 2.6e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                            Version #1.30
                             Length 188;
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    Indels
   0;
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Gaps
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RESULT 5 US-08-233-389C-3

Sequence

Sequence 3, Application US/08233389C Patent No. 5639855

GENERAL INFORMATION:

APPLICANT:
APPLICANT:

KANGAWA, Kenji MATSUO, Hisayuki ETO, Tanenao

Tanenao

ADRENOMEDULLIN

KITAMURA, Kazuo

ATTORNEY/AGENT INFORMATION:
NAME: HALLEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SH
TELECOMMUNICATION INFORMATION:

Qy

1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60

SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,389C

APPLICATION NUMBER: US/0: FILING DATE: 26-APR-1994 CLASSIFICATION: 530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

STREET: 122_
CITY: New York
CTATE: NY

10020

ADDRESSEE: C/O FISH aSTREET: 1251 Avenue of the Americas

CORRESPONDENCE ADDRESS: TITLE OF INVENTION: NUMBER OF SEQUENCES: 뫄 Ş В Ş DЬ Qy

1 ARLDVASEFRKKWNKWALSRGKRELRWSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60

; MOLECULE TYPE: US-09-004-713-1

protein

TOPOLOGY:

amino acid

185 amino acids

TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids

TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 596-9000 TELEFAX: (212) 596-9090

SHGN-5 DIV2 CON

ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHO

APPLICATION NUMBER: FILING DATE: JANUA CLASSIFICATION: 43

JANUARY 7, 1998

US/09/004,713

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

MEDIUM TYPE:

Floppy disk

Query Match 100.08; Best Local Similarity 100.08;

Matches

125;

Conservative

0;

Score 655; DB 2 Pred. No. 1e-72; Mismatches

DB 2; Length 185;

0;

Indels

Gaps

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RESULT 8
US-09-004-713-3
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                         Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                  121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                              82
                                                                                                                           61 DSSPDAARIRVKRYROSMNNFOGLRSFGCREGTCTVOKLAHQIYQETDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                 3, Application US/08486596A
5, 5837823
                                                                                                           ASIPDAARIRVKRYROSMNNFOGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10020
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                       93.3%;
                                                                                                                                                                                                                          Score 611; DB 2; I pred. No. 2.6e-67; 8; Mismatches 3;
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MOLECULE TYPE:
US-09-004-713-3
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Patent No. 5
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                                                                                                                                                                                                      Sequence 14,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTION PATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
NESTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                             TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                  APPLICANT: Smith, Derek L
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: Jack CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10020
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STATE: NY
                                                                                                                                                                                                                                                                                                          142 SPQGY 146
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                                                                                                                                                                                                                                                                                                                                          121 SPQGY 125
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                                                                                                                                                                                                                                                                                                                                                                           82 ASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKI 141
                                                                                                                                                                                                                                                                                                                                                                                             61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                STREET:
                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
Minneapolis
: MN
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1251 Avenue of the Americas
                                                                                                                                                                                                                        Application US/09070504
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                                E: Mueting, Raasch & Gebhardt, P.A.
119 No. 6268474th Fourth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                      Smith, Derek D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JANUARY 7, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%; Score 611; DB 2; 91.2%; Pred. No. 2.6e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 188;
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Length 50;

Indels

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Gaps

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RESULT 10
US-09-070-504-15
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Best Local Similarity 100.
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDERWEGO
                                                  TELEFAX: 612/305-1228 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                            REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smith, Derek | APPLICANT: Saha, Shankar APPLICANT: Abel, Peter W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 30-AP
                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 YRQSMNNFQGLRSFGCREGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 30-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: McCormack, My: REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                       McCormack, Myra H
                     CHARACTERISTICS: 50 amino acids
                                                                                                                                                                                                                                                                                                                  55401
                                                                                                                                                                                                                                                                                                                                                          Minneapolis
                                                                                                                                                                                                                                                                                                                                                MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09070504
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                                                                                                                                                                                        UMBER: US/09/070,504
30-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Derek D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Myra H
, Myra H
36,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.2%; Score 283; DB 4; 100.0%; Pred. No. 8.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/070,504
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                                                                                                          180.00020101
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                                                                                                                                                                                                                               Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                            RESULT 12
US-09-011-922A-3
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              Sequence 3, Application US/09011922A Patent No. 6320022 GENERAL INFORMATION:
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US-09-070-504-23
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TYRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-070-504-15
                                                                                                                                                                                        Matches
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
      APPLICANT:
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS: LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Saha, Shankar APPLICANT: Abel, Peter W.
                                                                                                                                     95 TYQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: li
                                                                                                                     1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 3 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3, Application US/09070504 6268474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Mueting, Raasch & Gebhardt,
119 No. 6268474th Fourth Street
Cuttitta, Frank; Martinez,
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                peptide
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                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                  24.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raasch & Gebhardt, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              36,602
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                                                                                                                                                                                     0,
                                                                                                                                                                                                  Score 163;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 231; DB 4;
Pred. No. 1.9e-21;
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2.2e-1 DB 4;

Length 31;

Indels

0;

Gaps

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Patent No.

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US-09-011-922A-3
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                                                                                           Sequence 14, Application US/09011922A Patent No. 6320022
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Best Local :
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Karen; Marricon: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN 6
                                                                               GENERAL INFORMATION:
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MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION UMBER: US/60/013,172
APPLICATION UMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/011,922,
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/I
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: HYPOTHETICAL:
                              APPLICANT:
                                                APPLICANT:
                                                               APPLICANT:
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OPERATING SYSTEM: MS WORD 9
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                           NAME/KEY: P072
OTHER INFORMATION: PreproAM(116-146)
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leslie A. Serunian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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J.; Hook, William; Walsh, Thomas; Grey,
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                             Cuttitta, Frank; Martinez,
Alfredo; Miller, Mae Jean; Unsworth, Ed
J.; Hook, William; Walsh, Thomas; Grey,
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                 Karen; Macri,
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No
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                  Charles
                                                                                                                                                                                                                                                                               Score 163; DB 4; pred. No. 2.2e-1
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     Role of
                                                      Unsworth, Edward
                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                   Sequence 7, Application US/09011922A Patent No. 6320022
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10154-000
ZIP: 10154-000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: MS WORD 97
                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION DATE: 17-rev --
FILING DATE: 17-rev --
PRIOR APPLICATION NUMBER: US/60/002,514
APPLICATION NUMBER: 18-Aug 1995
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TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
           APPLICANT: J.; HOOK,
APPLICANT: Karen; ME
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/60/013,172 FILING DATE: 12-Mar-1996 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/I FILING DATE: 16-Aug-1996 ATTORNEY/AGENT INFORMATION: NAME: Leslie A. Serunian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                        APPLICANT:
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CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/60/002,936 FILING DATE: 30-Aug-1995
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NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                OTHER INFORMATION: OTHER INFORMATION:
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31; Conservative
OF.
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345 Park Avenue
 SEQUENCES
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                                                                             Karen; Macri,
                                                                                       Cuttitta, Frank; Martinez, Alfredo; Miller, Mae Jean; J.; Hook, William; Walsh, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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16-Aug-1996
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100.0%; Pr
100.0%; O;
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Physiology
                             Adrenomedullin (AM) and the Gene-Related Product (PAMP) in Human Pathology and
                                                              Functional Role of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/09/011,922A
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                                                                            Charles
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                                                                                                 Thomas;
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Thomas; Grey,
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intact AM peptide
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RESULT 15
US-08-468-249A-20
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REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   Sequence 20, Application US/08468249A Patent No. 5886148
GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION UNBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION UNBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
                                                                                APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
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ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
COUNTRY: USA
ZIP: 02110-2804
                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PAMP-20
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SOFTWARE: ASCII
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                                                       Boston
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Leslie A. Serunian
Leslie A. Serunian
35,353
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                                                                   225 Franklin Street
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N-terminal
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100.0%; Pr
... 0;
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terminal 20 peptide
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Pred. No. 9.3e-07;
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                                                                                                                                              RECEPTOR AND DNA
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Search completed: October 17, 2002, 15:22:03 Job time: 8.55049 secs
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Best Local Similarity
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APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/07100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acid
                                                                                                                                                                                                                                                                                               TOPOLOGY: 1: MOLECULE TYPE:
                                                                  525 ATTNGHSQLPGHAKPGA 541
                                                                                                                                465 EVQABIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPP 524
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                               4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0:
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                      QDMKGASRSPEDSSPDA 66
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US-08-233-389C-3

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US-08-801-863-3

US-08-00-70-504-14

US-09-070-504-15

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US-09-011-922A-3

US-09-011-922A-7

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US-08-49-65-10

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Copyright (c) 1993 - 2002
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US-09-313-011-011-015-05-09-343-623-6 US-07-945-283-4 US-09-151-011-4 US-09-139-198A-4 US-09-039-198A-4 US-09-039-198A-4 US-09-039-198A-4 US-09-33-198A-4 US-08-163-14 US-08-98-15-14 US-08-113-921-3 US-08-113-93-366-6	ALIGN		ADRENOMEDULLIN 10 18: IS: IH & NEAVE IE of the America	.0.	, 38		Score Pred. ; Mism	SEFRKKW
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	tion	V: KURA, AWA, JO, E Tane	ON: CES: ODRES O FIS	E FOR Flopp PC C SM: entin	ABER: 26-AF: 26-AF: NFORM IMBER 3T NC 3T NC	SEC ID NO CTERISTIC amino ac acid inear protein	ty ervat	AFLGP
000000000000000000000000000000000000000	plicat	9855 MATION: KITAMURA KANGAWA, MATSUO, ETO, TAN	NVENTIC SEQUENCINCE AL SI C/C 1251 /	USA USA SADABLI PE: I IBM SYSTI Pate	ATE: (ATE: (TFOR SECUTARACTION OF TABLE OF THE TABLE OF TABL	Similarity 100 2; Conservative	WLGSLA
74. 87 87 87 87 87 87 87 87 87 87 87 87 87	SULT 1 -08-233-389C-1 Sequence 1, Ap	Tatent No. 5639855 GENERAL INFORMATION: APPLICANT: KITAMURA, APPLICANT: KANGAWA, APPLICANT: ETO, H	TITLE OF INVENTION: ADKEN TOWBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: C/O FISH & N STREET: 1251 Avenue of CITY: New York	STATE: NX COUNTRY: USA ZIP: 10020 COMPUTEN READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: TBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/08/233, FILING DATE: 26-APR-1994 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: HALEY Jr., James F. REGISTRATION NUMBER: 77,79 REFERENCE/DOCKET NUMBER: SHGN-TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: PERENA: (212) 566-9000 PETERNA: (212) 566-9000	INFORMATION FOR SEQ 1D NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 185 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein 08-233-389C-1	atch Sal	1 VSVALM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27, 94

REFERENCE/DOCKET NUMBER: SHGN-5 DIV3

TELEPHONE: (212) 596-9000

TELEPAX: (212) 596-9000

TELEFAX: (212) 596-9000

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                             APPLICANT: KITAMORA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
UNDRER OF SEQUENCES:
ADDRESSEE: C/O FISH & NEAVE
                                                                                                                                                                                                                               Sequence 1, Application US/08801863
Patent No. 5830703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 185 amino acids
amino acid
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Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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100.0%; Pred. No. 4.9e-99;
ive 0; Mismatches 0;
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1251 Avenue of the Americas
                                                                                  APPLICANT: KITAWURA, KAZUO
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, HISAYUKI
APPLICANT: MATSUO, HISAYUKI
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    Sequence 1, Application US/08486596A Patent No. 5837823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09004713; Patent No. 5910416
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KANGAWA, Kenji
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Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-596A-1
                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||
| FL 185
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                    US-08-486-596A-1
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                                                                                                                                                                                                                                                                   CITY: N
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RESULT 3
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61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.3%; Score 817; DB 1; Length 188;
89.1%; Pred. No. 2.2e-84;
.ive 10; Mismatches 9; Indels
  ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: ST.7794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 21,794
TELEPHONE: (212) 596-9000
TELEPHONE: (213) 596-9000
TELEPHONE: (218) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWRARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08801863
Patent No. 5830703
GENERAL INFORMATION:
APPLICANT: KINGAWA, Kenji
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: FTO, Tanenao
ITITE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 188 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.1%
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: CO
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US-08-801-863-3
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                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RFILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
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Patent No. 5639855
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAMA, Kenji
APPLICANT: RANGAMA, Kenji
APPLICANT: BTO, Tanenao
INVENTION: PINVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                          ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
                   APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
UNUMER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INRORAMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
MATSUO, Hisayuki
                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 185 amino acids
amino acid
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Best Local Similarity
                                                                                                                                                        CITY: New York
                                                                                                                                                                                                        USA
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FL 185
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US-08-233-389C-3
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1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                    US-09-004-713-3
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                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                      1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                               121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
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Best Local Similarity 89.1%; Pred. No. 2.2e-84;
Matches 156; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                            86.3%; Score 817; DB 2; Length 18
89.1%; Pred. No. 2.2e-84;
Live 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A
FILING DATE: UNR 7, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: SHGN-5 DIVI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: KTAMURA, KAZUO
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, HISAYUKI
APPLICANT: ETO, Tanenao
ITYLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08486596A Patent No. 5837823
            TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 188 amino Aniac Trees.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 188 amino acids
amino acid
                                                                                                                                                                                                                              Similarity 89.13
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                                                                                                                                                  , MOLECULE TYPE: protein US-08-801-863-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                        linear
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                                                                                                                                  TOPOLOGY:
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Best Local Simi
Matches 156;
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61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
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                                                                        64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFCCRFGTCTVQKLAHQ 123
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MEDIUM TYPE: Floppy disk
COMPUTER: IDN PC compatible
COMPUTER: TOWN PC compatible
COMPUTER: TOWN PC compatible
COMPUTER: TOWN PC compatible
COMPUTER: TOWN PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
CLASSIFICATION 1435
CLASSIFICATION 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.3%; Score 817; DB 2; L
89.1%; Pred. No. 2.2e-84;
tive 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: C/O FISH & NEAVE STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                  APPLICANT: KITAMORA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             Sequence 3, Application US/09004713
Patent No. 5910416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: SP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-900
TELEFAX: (212) 596-900
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 188 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-004-713-3
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Best Local Similarity
Matches 156; Conserv
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92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
CORRESPONDENCE ADDRESS:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCCOTMack, Myra H
REGISTRATION NUMBER: 36,602
REGISTRATION NUMBER: 36,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NAMBER: US/09/070,504 FILING DATE: 30-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 24.4%; Score 231; DB 4; L
Best Local Similarity 84.6%; Pred. No. 3.8e-19;
Matches 44; Conservative 3; Mismatches 3;
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                                                                                                                                                                                                                          180.00020101
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/09070504 Patent No. 6268474
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NAME: MCCAFMECK, Myra H
REGISTRATION NUMBER: 36,602
REPRENCE/DOCKET NUMBER: 180.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                REFERENCE POCKET NUMBER: 180.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-070-504-15
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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STATE: MI
COUNTRY:
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                                         Sequence 14, Application US/09070504
Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Santh, Derek D.
APPLICANT: Santh, Derek D.
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Reasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
STATE: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-070-504-15
Sequence 15, Application US/09070504
Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Sala, Shankar
APPLICANT: Sala, Shankar
APPLICANT: BABI, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION WHERE: US/09/070,504
FILING DATE: 30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 6268474th Fourth Street CITX: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: MCCOTMaCk, Myra H
REGISTATION UNDBER: 36,602
REFERENCE/DOCKET NUMBER: 180.0
TELECOMMUNICATION INFORMATION:
TELEFAX: 612/305-1220
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                                                                                                                                                                                                               USA
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                   US-09-070-504-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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Gaps

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APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: Alfredo; Miller, Malsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
Annumeron.
    113 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
COMPUTER: ASCII
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
FILING DATE: 18-AUG-1995
FILING DATE: 18-AUG-1995
FILING DATE: 30-AUG-1995
FILING DATE: 30-AUG-1995
FILING DATE: 30-AUG-1995
FILING DATE: 30-AUG-1995
FILING DATE: 12-MAI-1996
FILING DATE: 16-AUG-1996

                                         1 TVOKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                                                                                                                                                                                                                                                                Sequence 14, Application US/09011922A Patent No. 6320022 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35.353
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy Disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 31; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
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COTHER INFORMATION:
US-09-011-922A-14
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3Y: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                         RESULT 13
US-09-011-922A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cutilita, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen: Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31;
                                                                                   Indels
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17.2%; Score 163; DB 4; I
100.0%; Pred. No. 9.2e-12;
iive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 9.2e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               113 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PALLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug 1995
FILING DATE: 18-Aug 1995
FILING DATE: 30-Aug 1995
FILING DATE: 30-Aug 1995
FILING DATE: 30-Aug 1995
FILING DATE: 30-Aug 1995
FILING DATE: 12-Mar 1996
FILING DATE: 12-Mar 1996
FILING DATE: 16-Aug 1996
ATIONENEY 16-Aug 1996
ATIONENEY AGENT 10-Aug 1996
AUG 1996
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; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3
                                                                                                                                                                                                             1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 345 Park Avenue
New York
                                                                                   31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 345
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                                                                                        Matches
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                                                           Length 31;
Synthetic homolog of
two-thirds of the intact AM peptide
                                                                                            Indels
                                                           17.2%; Score 163; DB 4; 100.0%; Pred. No. 9.2e-12; ive 0; Mismatches 0;
                                                                                                                             113 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
                                                                                                                                            1 TVOKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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SEQ ID NO 2
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                                                                               Patent No. 6320022

GENERAL INFORMATION:
APPLICANT: Cutilita, Frank; Martinez,
APPLICANT: Cutilita, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
TITLE OF INVENTION: Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%; Score 107; DB 4; Length 20; 100.0%; Pred. No. 1e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-ANG-1996
ATTORNEY AGENT INFORMATION:
NAME: Leslie A. Serunian:
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4202US3
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Proadrenomedullin N-OTHER INFORMATION: terminal 20 peptide US-09-011-922A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-Feb-1998
PRIOR APPLICATION NUMBER: 05/00/02,514
APPLICATION NUMBER: 05/00/02,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/00/02,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION NUMBER: 05/00/13,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
                                       Sequence 7, Application US/09011922A Patent No. 6320022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZOPINITI CONTROLL OF THE STATE 
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HYPOTHETICAL: NO
FRAGMENT TYPE: N-termin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Local Sim
20;
US-09-011-922A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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Gaps

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APPLICANT: STUTZMAN-ENGWALL, KIM J.
APPLICANT: STUTZMAN-ENGWALL, KIM J.
APPLICANT: PRICE, BRENDA S.
TITLE OF INVENTION: STREPTOMYCES AVERMITILIS REGULATORY GENES FOR INCREASED
TITLE OF INVENTION: AVERMECTIN PRODUCTION
FILE REPERBNCE: PC9944A
CURRENT APPLICATION NUMBER: 05/09/390,721
CURRENT FILING DATE: 1999-09-07
EARLIER FILING DATE: 1999-09-07
EARLIER FILING DATE: 1988-09-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATCHIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 ERLRIARELHDVVTHSMGLIAVKVGVANHVLHIRPQEAYDALQVIERTSRTALN-DMRRM 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 SPGLLLIGFAALLGA--------WQLGRAARQRRAFAVRAAEQLAQRAVTE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 LGVLRTSEGEROSAALGPLPGALALPDLVGQAGAQLTMRGVESLPDGVALAVYRIVQEAL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 ------SYPTGLADVKAGPAQTL--IRPQDMKGASRSPEDSSPDAARIRVKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.1%; Score 86.5; DB 4; Length 401; Best Local Similarity 20.5%; Pred. No. 0.12; Matches 52; Conservative 26; Mismatches 83; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 DNVA-----PRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 RQSMNNFQGLR---SFGCRFGTCTVQKLAHQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: October 17, 2002, 15:22:04
Job time : 13.4495 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Streptomyces avermitilis US-09-390-721-2
RESULT 15
US-09-390-721-2
; Sequence 2, Application US/09390721
; Patent No. 6197591
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 ---APAPPSGSAPH 180
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October 17, 2002, 14:45:20; Search time 4.53865 Seconds (without alignments) 279.848 Million cell updates/sec
                                                                                                                                                                                          US-10-018-924-2_COPY_95_146
283
1 YRQSMNNFQGLRSFGCRFGT......FTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                231628
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                 231628 seqs, 24425594 residues
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                          Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCCOTMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEFHONE: 612/305-1220
TELEFHONE: 612/305-1220
TELEFAX: 612/305-1220
TELEFAX: 612/305-1220
SEQUENCE CHARACTERISTICS:

52 amino acids

amino acid

STRANDEDESS: Single TOPOLOGY: linear MOLECULE TYPE: peptide US-09-070-504-14

ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 6268474th Fourth Street CITY: Minneapolis STATE: MN

55401

COUNTRY:

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ID	US-09-070-504-14	US-08-233-3890-1	US-08-801-863-1	US-08-486-596A-1	US-09-004-713-1	US-08-233-389C-3	US-08-801-863-3	US-08-486-596A-3	US-09-004-713-3	US-09-070-504-15	US-09-070-504-23	US-09-011-922A-3	US-09-011-922A-14	US-09-011-922A-2	US-08-265-628-2	US-07-891-942G-10	US-07-891-942G-8	US-08-370-909-19	US-08-504-048-8	US-08-540-922D-12	US-07-891-942G-5	US-08-966-388-4	US-09-188-403-4	US-09-188-404-4	US-09-281-259-4	US-08-934-222-17	US-08-933-402-17
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Lengt)	5,5	186	185	185	185	188	188	188	188	2	31	31	33	13	828	508	529	529	529	537	260	775	775	775	775	10	10
Query	100.0	100.0	100.0	100.0	100.0	97.9	97.9	97.9	97.9	81.6	57.6	57.6	57.6	20.1	19.8	18.7	18.7	18.7	18.7	18.7	18.7	18.4	18.4	18.4	18.4	18.0	18.0
Score	283	283	283	283	283	277	277	277	277	231	163	163	163	22	26	53	53	53	23	.53	23	25	52	25	25	51	51
Result No.	-	7	e	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27
	Query Score Match Length DB ID	Score Match Length DB ID Description 283 100.0 52 4 US-09-070-504-14	Score Match Length DB ID Description 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-333-3804-1	Score Match Length DB ID Description 283 100.0 185 1 US-08-273-3892-1 Sequence 14, 283 100.0 185 1 US-08-83-3-896-1 Sequence 1, 283 100.0 185 1 US-08-83-100.0 185 1 US-08-801-863-1	Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 Sequence 1, 283 100.0 185 2 US-08-86-596A-1 Sequence 1, 283 100.0 185 2 US-08-486-596A-1 Sequence 1, 283 100.0 185 2 US-08-486-596A-1	Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 Sequence 1, 283 100.0 185 2 US-08-801-863-1 Sequence 1, 283 100.0 185 2 US-08-801-863-1 Sequence 1, 283 100.0 185 2 US-08-901-86-596A-1 Sequence 1, 283 100.0 185 2 US-08-901-86-596A-1 Sequence 1, 283 100.0 185 2 US-09-004-713-1	Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 Sequence 1, 283 100.0 185 2 US-08-801-863-1 Sequence 1, 283 100.0 185 2 US-08-486-596A-1 Sequence 1, 283 100.0 185 2 US-09-004-713-1 Sequence 1, 277 97.9 188 1 US-08-238-389C-3	Score Match Length DB ID Description 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 Sequence 1, 283 100.0 185 2 US-08-486-596A-1 Sequence 1, 283 100.0 185 2 US-09-004-713-1 Sequence 1, 277 97.9 188 1 US-08-233-389C-3 Sequence 2, 277 97.9 188 2 US-08-801-863-3 Sequence 2, 277 97.9 188 2 US-08-801-863-3 Sequence 3, 277 97.9 188 2 US-08-801-863-3 Sequence 2, 277 97.9 188 2 US-08-801-863-3 Sequence 3, 277 97.9 188 1 US-08-8	Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 Sequence 17, 283 100.0 185 2 US-08-801-863-1 Sequence 17, 283 100.0 185 2 US-08-486-596A-1 Sequence 17, 283 100.0 185 2 US-08-486-596A-1 Sequence 17, 283 100.0 185 2 US-08-801-803-3 Sequence 17, 277 97.9 188 1 US-08-233-389C-3 Sequence 3, 277 97.9 188 2 US-08-486-596A-3 Sequence 3, 277 97.9 188 2 US-08-486-596A-3 Sequence 3, 277 97.9 188 2 US-08-486-596A-3	Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14 283 100.0 185 1 US-08-233-389C-1 Sequence 14 283 100.0 185 2 US-08-801-863-1 Sequence 17 283 100.0 185 2 US-08-801-863-1 Sequence 17 283 100.0 185 2 US-09-004-713-1 Sequence 17 277 97.9 188 2 US-08-801-863-3 Sequence 3, 277 277 97.9 188 2 US-09-004-713-3	Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14. 283 100.0 185 1 US-08-233-389C-1 Sequence 1, 283 100.0 185 2 US-08-801-863-1 Sequence 1, 283 100.0 185 2 US-09-004-713-1 Sequence 1, 277 97.9 188 2 US-09-004-713-1 Sequence 1, 277 97.9 188 2 US-08-8863-3 Sequence 3, 277 97.9 188 2 US-08-8863-3 Sequence 3, 277 97.9 188 2 US-08-8863-3 Sequence 3, 277 97.9 188 2 US-09-004-713-3 Sequence 3, 27	Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 Sequence 14, 283 100.0 185 2 US-08-801-863-1 Sequence 1, 283 100.0 185 2 US-08-486-596A-1 Sequence 1, 283 100.0 185 2 US-08-486-596A-1 Sequence 1, 277 97.9 188 2 US-08-486-596A-3 Sequence 3, 277 97.9 188 2 US-09-004-713-3 Sequence 3, 277 97.9 188 2 US-09-004-713	Query Guery 283 100.0 52 4 US-09-070-504-14 Sequence 14 283 100.0 185 1 US-08-233-389C-1 Sequence 14 283 100.0 185 2 US-08-801-863-1 Sequence 14 283 100.0 185 2 US-08-801-863-1 Sequence 14 283 100.0 185 2 US-08-801-863-1 Sequence 17 277 97.9 188 1 US-08-233-389C-3 Sequence 17 277 97.9 188 2 US-08-801-863-3 Sequence 3 277 97.9 188 2 US-08-801-863-3 Sequence 3 277 97.9 188 2 US-09-801-863-3 Sequence 3 277 97.9 188 2 US-09-004-713-3 Sequence 3 277 97.9 188 2 US-09-004-713-3 Sequence 3 277 97.9 188 2 US-09-004-713-3 Sequence 3	Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14. 283 100.0 185 1 US-08-233-389C-1 Sequence 1, 283 100.0 185 2 US-08-801-863-1 Sequence 1, 283 100.0 185 2 US-09-004-713-1 Sequence 1, 277 97.9 188 2 US-09-004-713-1 Sequence 2, 277 97.9 188 2 US-09-004-713-3 Sequence 3, 277 97.9 188 2 US-09-001-928-4-15 Sequence 15, 278 97.9 188 2 US-09-001-928-4-15 Sequence 15, 278 97.9 188 2 US-09-010-928-4-15 Sequence 15, 278 97.9 188 97.6 91.9228-4-14 Sequence 15, 288 97.6 91.9228-4-14 Seq	Ouery Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 283 100.0 185 1 US-08-233-389C-1 283 100.0 185 2 US-08-801-863-1 283 100.0 185 2 US-08-801-863-1 283 100.0 185 2 US-08-801-863-1 284 100.0 185 2 US-08-801-863-1 287 97.9 188 2 US-08-233-389C-3 277 97.9 188 2 US-08-801-863-3 277 97.9 188 2 US-08-801-863-3 277 97.9 188 2 US-09-04-713-3 278 81.6 50 4 US-09-070-504-15 2890ence 3, 290-04-713-3 281 81.6 50 4 US-09-070-504-15 281 81.6 50 4 US-09-070-504-15 282 820ence 2, 205-09-070-504-15 282 820ence 2, 205-09-070-504-15 282 820ence 2, 205-09-070-504-15 282 820ence 2, 205-09-070-504-23 282 820ence 2, 205-09-071-9228-2	Core Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 283 100.0 185 1 US-08-233-389C-1 Sequence 14, 283 Sequence 14, 283 Sequence 17, 283 Sequence 27, 277 Sequence 27, 277 Sequence 3, 277 Sequence 15, 277 Sequence 3, 277 Sequence 3, 277 Sequence 15, 277 Sequence 15, 277 Sequence 2, 277 Sequence	Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14. 283 100.0 185 1 US-08-233-389C-1 Sequence 14. 283 100.0 185 2 US-08-801-863-1 Sequence 1, 283 100.0 185 2 US-09-004-713-1 Sequence 1, 283 100.0 185 2 US-09-004-713-1 Sequence 1, 277 97.9 188 2 US-09-004-713-3 Sequence 2, 277 97.9 188 2 US-09-004-713-3 Sequence 2, 277 97.9 188 2 US-09-004-713-3 Sequence 3, 277 97.9 188 2 US-09-004-713-3 Sequence 3, 277 97.9 188 2 US-09-004-713-3 Sequence 3, 277 97.9 188 2 US-09-004-713-3 Sequence 2, 277 97.9 188 2 US-09-001-9228-3 Sequence 1, 278 97.6 31 4 US-09-011-9228-3 Sequence 1, 278 97.9 188 2 US-09-011-9228-3 Sequence 1, 278 97.9 188 2 US-09-011-9228-3 Sequence 2, 278 97.9 188 2 US-09-011-9228-3 Sequence 2, 278 97.9 188 2 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297 97.9 188 2 US-09-004-713-3 28quence 2, 28-09-004-713-3 28quence 2, 31 4 US-09-011-922A-3 28quence 2, 31 4 US-09-011-922A-3 28quence 2, 20-09-011-922A-3 28quence 2, 20-09-011-92A-3 28quence 2, 20	Ouery Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 283 100.0 185 2 US-08-081-853-1 Sequence 1, 283 100.0 185 2 US-08-04-713-1 Sequence 1, 283 100.0 185 2 US-09-004-713-1 Sequence 1, 277 97.9 188 1 US-08-233-389C-3 Sequence 2, 277 97.9 188 2 US-08-081-863-3 Sequence 3, 277 97.9 188 2 US-08-046-596A-3 Sequence 3, 277 97.9 188 2 US-09-040-713-3 Sequence 2, 277 97.9 188 2 US-09-040-713-3 Sequence 1, 163 57.6 31 4 US-09-071-922A-3 Sequence 1, 163 57.6 31 4 US-09-071-922A-3 Sequence 1, 163 57.6 31 4 US-09-011-922A-3 Sequence 2, 25 19.8 858 2 US-08-08-265-628-2 Sequence 1, 25 18.7 508 1 US-07-891-942G-10 Sequence 1, 25 18.7 529 1 US-07-891-942G-8 Sequence 1, 25 18.7 529 2 US-08-20-18 Sequence 1, 25 18.7 529 1 US-07-891-942G-8 Sequence 1, 25 18.7 529 2 US-08-20-18 Sequence 1, 25 18.7 520 1 US-08-20-18 Seq	Query Score Match Length DB ID 283 100.0	Ouery Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14. 283 100.0 185 1 US-08-233-389C-1 283 100.0 185 2 US-08-801-863-1 284 100.0 185 2 US-09-004-713-1 287 97.9 188 2 US-08-801-863-3 277 97.9 188 2 US-08-801-863-3 277 97.9 188 2 US-08-801-863-3 277 97.9 188 2 US-09-004-713-3 277 97.9 188 2 US-09-011-922A-3 28quence 2, Sequence 2, Sequence 14, Sequence 2, US-09-011-922A-3 28quence 2, Sequence 2, US-09-011-922A-1 28	Query Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 283 100.0 185 2 US-08-081-863-1 Sequence 1, 283 100.0 185 2 US-08-04-713-1 Sequence 1, 283 100.0 185 2 US-08-04-713-1 Sequence 1, 277 97.9 188 1 US-08-233-389C-3 Sequence 2, 277 97.9 188 2 US-08-081-863-3 Sequence 3, 277 97.9 188 2 US-08-046-596A-3 Sequence 3, 277 97.9 188 2 US-09-040-713-3 Sequence 2, 277 97.9 188 2 US-09-040-713-3 Sequence 2, 277 97.9 188 2 US-09-041-92A-15 Sequence 1, 163 57.6 31 4 US-09-011-922A-3 Sequence 1, 163 57.6 31 4 US-09-011-922A-3 Sequence 2, 25 19.8 858 2 US-08-04-048 Sequence 1, 25 18.7 509 1 US-07-891-942G-10 Sequence 1, 25 18.7 51 18.7 51 18.7 529 1 US-07-891-942G-10 Sequence 1, 25 18.7 51	Query Score Match Length DB ID 283 100.0	Ouery Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 Sequence 14, 283 100.0 185 2 US-08-801-863-1 Sequence 1, 283 100.0 185 2 US-08-801-863-1 Sequence 1, 283 100.0 185 2 US-09-004-713-1 Sequence 1, 277 97.9 188 2 US-08-801-863-3 Sequence 2, 277 97.9 188 2 US-09-004-713-3 Sequence 2, 277 97.9 188 2 US-08-801-863-3 Sequence 2, 277 97.9 188 2 US-09-004-713-3 Sequence 2, 277 97.9 188 2 US-09-004-713-3 Sequence 2, 277 97.9 188 2 US-09-004-713-3 Sequence 2, 277 97.9 188 2 US-09-0104-713-3 Sequence 2, 277 97.9 188 2 US-09-011-922A-3 Sequence 1, 278 97.6 31 4 US-09-011-922A-3 Sequence 2, 278 97.6 31 4 US-09-011-922A-3 Sequence 2, 278 97.8 18.7 529 1 US-07-891-942G-10 Sequence 1, 278 18.7 529 2 US-08-56-528-2 Sequence 1, 278 18.7 529 2 US-08-504-048-8 Sequence 2, 28-08-504-048-8 Sequence 4, 28-08-504-048-8 Sequence 4, 28-08-504-048-8 Sequence 6, 28-08-504-048-8 Seq	Query Score Match Length DB ID 283 100.0 52 4 US-09-070-504-14 Sequence 14, 283 100.0 185 1 US-08-233-389C-1 283 100.0 185 2 US-08-081-863-1 Sequence 1, 283 100.0 185 2 US-08-081-863-1 Sequence 1, 283 100.0 185 2 US-08-081-863-3 Sequence 1, 277 97.9 188 1 US-08-233-389C-3 Sequence 2, 277 97.9 188 2 US-08-081-863-3 Sequence 3, 277 97.9 188 2 US-08-081-863-3 Sequence 3, 277 97.9 188 2 US-09-040-713-3 Sequence 2, 277 97.9 188 2 US-09-040-713-3 Sequence 2, 277 97.9 188 2 US-09-040-713-3 Sequence 2, 277 97.9 188 2 US-09-011-922A-3 Sequence 1, 278 97.9 188 2 US-09-011-922A-3 Sequence 2, 278 97.9 188 2 US-09-011-922A-3 Sequence 2, 278 97.9 188 2 US-09-011-922A-3 Sequence 2, 278 97.9 188 2 US-08-265-628-2 Sequence 1, 278 97.9 188 2 US-08-265-628-2 Sequence 1, 278 97.9 188 7 S50 1 US-07-891-942G-8 Sequence 1, 278 18.7 550 1 US-07-891-942G-8 Sequence 2, 278 18.7 550 1 US-07-891-942G-5 Sequence 2, 278 18.7 550 1 US-07-891-942G-5 Sequence 2, 278 18.4 775 2 US-08-504-048-8 Sequence 2, 278 18.4 775 4 US-09-188-403-4 Sequence 4, 252 18.4 775 4 US-09-188-203-17 Sequence 4, 252 18.4 775 4 US-08-50-17 Sequence 4, 252 18.4 775 4 US-08-50-18 Sequence 4, 252 18.4 775 4 US-08-50-17 Sequence 4, 252 18.4 775 4 US-08-50-18 Sequence

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Gaps

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1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY

Query Match
100.0%; Score 283; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 8e-35;
Matches 52; Conservative 0; Mismatches 0; Indels

Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl			GRP-RECEPTOR OF USE
US-09-207-621-17 US-08-532-818-17 US-09-231-797-17 US-08-934-224-17 US-08-934-23-17 US-08-934-23-17	-413-492 -439-313 -318-831 -290-731 -290-731 -290-731 -797-366 -956-268 -470-179	ALIGNMENTS 070504	rek D. nkar er W. PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF USE 2.3
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18.0 18.0 18.0 18.0	18.0 17.7 17.7 17.7 17.7 17.7 17.3 17.3 17.0	4 Applicat 68474	
51 51 51 51 51	51 50 50 50 50 50 50 50 64 64 64 64 7.5	RESULT 1 US-09-070-504-14 : Sequence 14, Appli : Patent No. 6268474	GENERAL INFORMATION: APPLICANT: Smith, APPLICANT: Saha, APPLICANT: Abel, TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD
33310 335 337	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT US-09-0; ; Sequen	GENE APP APP APP APP APP APP APP APP APP AP

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
TELEFAX: (212) 596-9000
TELEFAX: (212) 596-9000
TELEFAX: (112) 596-9000
TELEFAX: (110) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 283; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 52; Conservative 0; Mismatches 0;
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEX Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
TELECOMMUNICATION INFORMATION: TELEPAX: (212) 596-9000
TELEPAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08486596A
Patent No. 5837823
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KATAMURA, Kenji
APPLICANT: RANGAWA, Kenji
APPLICANT: ETO, Tamenao
TITLE OF INVENTION: ADEROMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: c/o FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 185 amino acids
amino acid
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CITY: New York
STATE: NY
COUNTR: USA
21P: 10020
COMPUTER READABLE FORM:
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US-08-486-596A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPLLCATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 283; DB 1;
illarity 100.0%; Pred. No. 3.8e-34;
Conservative 0; Mismatches 0;
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US-08-801-863-1
Sequence 1, Application US/08801863
PREACH NO. 5830703
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KATAMORA, Kenji
APPLICANT: ETO, Tanenao
TILLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Average
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: C/O FISH & NEAVE STREET: 1251 Avenue of the Americas CITY: New York STATE: NY
                                                                                                                                                                                                 APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGANA, Kenji
APPLICANT: KANGANA, Kenji
APPLICANT: ETO, Tanenao
TITILE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                             Sequence I, Application US/08233389C Patent No. 5639855 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 185 amino acids
amino acid
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Matches 52; Conserva
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US-08-486-596A-1

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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Gaps

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Score 277; DB 1;
Pred. No. 3e-33;
0; Mismatches
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GENERAL INFORMATION
APPLICANT: KITAMURA, KAZUO
APPLICANT: KARNAWA, KENJI
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELERONE: (212) 596-9000
TELERON: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                           APPLICATION .....
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPRAX: (212) 596-9000
TELERATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 188 antino acids
TYPE: amino acid
                 1251 Avenue of the Americas
                                                       STATE: NY
COUNTRY: USA
ZIP. 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08801863
Patent No. 5830703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 97.9%;
Best Local Similarity 98.1%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                        New York
                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-801-863-3
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                                                                                                          Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 185;
                                                                                    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JI., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INFORMATION:
MET POWNING ATTON INFORMATION:
100.0%; Score 283; DB 2; 100.0%; Pred. No. 3.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 283; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 52; Conservative 0; Mismatches 0;
                                              0; Mismatches
                                                                                                                                                                                                                            Sequence 1, Application US/09004713
Patent No. 5910416
GENERAL INFORMATION:
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: MATSUO, Hisayuki
TITLE OF INVENTION: ADBENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08233389C
Patent No. 5639855
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 185 amino acids TYPE: amino acid
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-004-713-1
                    Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                            US-09-004-713-1
    Query Match
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                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 277; DB 2; Length 188;
Pred. No. 3e-33;
0; Mismatches 1; Indels
                                                                                                                                  Score 277; DB 2; Length 188; Pred. No. 3e-33; 0; Wismatches 1; Indels
                                                                                                                                                                                                                 1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/486,596A
FILING DATE: UNBER: US/08/486,596A
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: HALEY IT., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08486596A
Patent No. 5837823
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KATAMURA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: MATSUO, Hisayuki
APPLICANT: APSUO, Hisayuki
APPLICANT: BTO, Tamenao
TITLE OF INVENTION: ADBENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09004713 Patent No. 5910416 GENERAL INFORMATION:
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illarity 98.1%;
Conservative (
                                                                                                                                    Query Match
Best Local Similarity 98.1%;
Matches 51; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KITAMURA, Kazuo
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-801-863-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-486-596A-3
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10020
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Sequence 15, Application US/09070504

Sequence 15, Application US/09070504

Patent No. 6266474

Patent No. 6266476

PAPPLICANT: Smith, Derek D.

APPLICANT: Saha, Shankar

APPLICANT: Abel, Peter W.

TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                       COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
ATTORNEY/AGBWT INFORMATION:
NAME: HALEY JT., James F.
REGISTRATION NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INDER: 3600000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....nure:SEEE: Mueting, Raasch & Gebhardt, P.A STREET: 119 No. 6268474th Fourth Street CITY: Minneapolis COUNTRY: USA 770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 277; DB 2;
Pred. No. 3e-33;
0; Mismatches
                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
APPLICANT: MATSUO, HISAYUKI
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.9%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 188 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-004-713-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                          USA
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GENERAL INFORMATION:
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Tracen; Macri, Charles
APPLICANT: Raren; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.6%; Score 163; DB 4; Length 31; 100.0%; Pred. No. 2.2e-17; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NAME: US/09/011,922A
FILING DATE: 17-Feb-1998
FILING DATE: 17-Feb-1998
FILING DATE: 18-Ray-1995
FILING DATE: 18-Ray-1995
FILING DATE: 18-Ray-1995
FILING DATE: 30-Ray-1995
FILING DATE: 30-Ray-1995
FILING DATE: 12-Ray-1996
FILING DATE: 16-Ray-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ): OTHER INFORMATION: Preproam(116-146)
  1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                           Sequence 3, Application US/09011922A
Patent No. 6320022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS WORD 97 SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.69
Best Local Similarity 100.0
Matches 31; Conservative
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ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                             US-09-011-922A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/09070504

Patent No. 6268474

GENERAL INFORMATION:
APPLICANT: Saha, Shankar
APPLICANT: Saha, Shankar
APPLICANT: AD61, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF GERP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                               Score 231; DB 4; Length 50; Pred. No. 3.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
NAME: MCCOTMack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MCCCTMaCk, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERLSTICS: LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                 81.6%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-070-504-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 31; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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RESULT 13

TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

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APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Addrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.1%; Score 57; DB 4; Length 13; 100.0%; Pred. No. 0.034; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4202US3
TELECOMNUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
SCETMARE: ASCII
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION NUMBER: US/60/013,172
FILING DATE: 13-Aug-1996
PRIOR APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION NUMBER: US/60/013,172
FILING DATE: 16-Aug-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
NUMBER: LESLIG ALGERIAN
                                                                                                                                                                                                                                                                                                                                                                            MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINN
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 amino acids
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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                          Sequence 14, Application US/09011922A

Patent No. 6320022

GENERAL INFORMATION:
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo: Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen: Macri, Charles
ITILE OF INVENTION: Functional Role of
ITILE OF INVENTION: Product (PAMP) in Human Pathology and
ITILE OF INVENTION: Physiology
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADRESSEE:
ADDRESSEE:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.6%; Score 163; DB 4; Length 31; Best Local Similarity 100.0%; Pred. No. 2.2e-17; Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic homolog of two-thirds of the intact AM peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/US96/13286
FILING DATE: 16-Aug-1996
FILING DATE: 16-Aug-1996
ATCHNEY/AGENT INFORMATION:
ANAWEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2026-4202US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORGAN & FINNEGAN, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10154-0053
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
COTHER INFORMATION:
US-09-011-922A-14
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US-09-011-922A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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Sequence 2, Application US/09011922A Patent No. 6320022 GENERAL INFORMATION:

RESULT 14 US-09-011-922A-2

1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

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NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAnderews, Held 6 Malloy, itd.

STREET: 500 Wadison St. Suite 3400

STATE: 111Anois

CONFUTER READALE FORM:

COMPUTER READALE FORM:

MEDIUM TYPE: 110Ppy disk

COMPUTER: 18M FC Compatible

COMPUTER: 18M FC Compatible

SOTTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/265,628

FILING DATE:

CLASSITICATION: 435

REDISTRATION: 435

REDISTRATION: 435

REDISTRATION: 435

REDISTRATION NUMBER: US/07/959,945

FILING DATE:

APPLICATION NUMBER: 1050/847,564

FILING DATE:

MANG: 1050/106/107

FELEPAR: 111-707-915

MATORNEY/AGENT INFORMATION:

REDISTRATION NUMBER: 130,107

FELEPAR: 131-707-915

MATORNEY/AGENT INFORMATION:

REDISTRATION NUMBER: 130,107

FELEPAR: 131-707-915

MATORNEY/AGENT: 1989

FELEPAR: 131-707-915

MATORNEY/CREATION NUMBER: 130,107

MATORNEY/CREATION NUM
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Search completed: October 17, 2002, 14:48:43 Job time : 5.53865 secs

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Sequence 15,

Sequence Sequence Sequence 6

US-09-141-206-2 US-09-107-149-2 US-09-107-149-17 US-08-972-927-6 US-08-968-752B-6

US-08-207-904-15

Appl Appli Appli Appli Appl Appl

Sequence Sequence Sequence

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US-08-265-628-2 US-08-423-459-10 US-08-423-752-10 US-08-945-994-3 US-09-364-31-24 US-09-414-006-10 US-09-247-155-174 US-09-141-266-10 US-09-141-206-7 US-09-141-206-7

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                                                                                                                    October 17, 2002, 14:45:20; Search time 3.49127 Seconds (without alignments) 279.848 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1,
Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1,
Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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                                                                                                                                                                                                    US-10-018-924-2_COPY_107_146
219
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-801-89C-3

US-08-801-89C-3

US-08-004-713-3

US-09-004-713-3

US-09-007-504-15

US-09-011-922A-3

US-09-011-922A-14

US-09-011-922A-14

US-09-011-922A-14

US-09-011-922A-14

US-09-011-922A-14

US-09-188-403-4

US-09-188-403-4

US-09-188-403-4

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US-09-188-403-4

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US-09-188-403-4

US-09-231-797-17
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US-08-486-596A-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Query
Match Length DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                    Sequence:
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                                                                                                                        Run on:
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                                                          GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Saha, Shankar
APPLICANT: Saha, Shankar
TITLEOF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/070,504
FILING DATE: APPRICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 219; DB 4; Best Local Similarity 100.0%; Pred. No. 3.6e-26; Matches 40; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MCCormack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                  Sequence 14, Application US/09070504 Patent No. 6268474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELETAX: 012/305-1228
TELETAX: 612/305-1228
INFORMATION FOR SEQ 1D NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                        USA
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US-09-070-504-14
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Sequence Sequence

Sequence

US-08-934-223-17 US-09-413-492-17

Sequence

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                 OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NORMER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION OF 1: 596-9000
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHRRACTERISTICS:
LENGTH: 185 amino acids
TOPPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A FILING DATE: UND 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 SFGCRFGTCTVQKLAHQIYQFTDKDKDKNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 219; DB 2;
ilarity 100.0%; Pred. No. 1.6e-25;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
TELECOMMUICATION INFORMATION:
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: c/o FISH & NEAVE
F: 1251 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08486596A
Patent No. 5837823
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA ZIP: 10020 COMPUTER READABLE FORM:
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COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-486-596A-1
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STATE:
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Ouery Match

100.0%; Score 219; DB 1; Length 185;

Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 40; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIP: 10020
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC DOS/MS-DOS
OPFRATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PATENTIN PCT DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,389C
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INPORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION SEQ ID NO: 1:
TELEPHONE: (212) 566-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                        APPLICANT: KITAMORA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08801863
Patent No. 5830703
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: TO Tanemao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                       Sequence 1, Application US/08233389C Patent No. 5639855 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-233-389C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                   US-08-233-389C-1
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Gaps

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Length 188;
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                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,389C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 213; DB 1; L
Pred. No. 1.3e-24;
0; Mismatches 1;
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FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 57,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 12,596-9000
TELECRAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
ATTORNEY AGENT INPORMATION:
NAME: HALEY Jr., James F.
REGISTATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFERX: (212) 596-9000
TELEFERX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
                1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAMA, Kenji
APPLICANT: KANGAMA, Kenji
APPLICANT: ETO, Tanenao
TITILE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08801863
Patent No. 5830703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.3%;
Best Local Similarity 97.5%;
Matches 39; Conservative (
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-233-389C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                     New York
                                                                                  USA
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                                                                             COUNTRY: US
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                                                        Gaps
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         Length 185;
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                                                   Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENY APPLICATION DATA:

APPLICATION NUMBER: US/09/004,713

FILING DATE: JANUARY 7, 1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HALEY JF., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON

TELEPHONE: (212) 596-9000

TELEPHONE: (212) 596-9000

TELEFERAL (212) 596-9000

INFORMATION FOR SED ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: MAIN ORGAGE

TYPE: amino acid
                                                                                                                   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
100.0%; Score 219; DB 2;
100.0%; Pred. No. 1.6e-25;
live 0; Mismatches 0;
                                                                                         1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 219; DB 2; Best Local Similarity 100.0%; Pred. No. 1.6e-25; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                              Sequence 1, Application US/09004713
Patent No. 5910416
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08233389C
Patent No. 563985
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KITAMURA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: MATSUO, Hisayuki
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C/O FISH & NEAVE
                         Best Local Similarity 100.
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-004-713-1
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US-08-233-389C-3
                                                                                                                                                                                                                           US-09-004-713-1
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    Query Match
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KANGAWA, Kenji

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APPLICANT:
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                                                                                                                        Score 213; DB 2; Length 188;
Pred, No. 1.3e-24;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: 03/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 213; DB 2;
Pred. No. 1.3e-24;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION UNBER: 27,794
REFERENCE/DOCKET NUMBER: 516N-5 DIVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08486596A
Patent No. 5837823
GENERAL INPORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: KANGAWA, Kenji
APPLICANT: HATSUO, Hisayuki
APPLICANT: HATSUO, Hisayuki
APPLICANT: HATSUO, Tanenao
TITLE OF INVENTION: ADRENOMEDULIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-004-713-3
; Sequence 3, Application US/09004713
Patent No. 5910416
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.5%;
Matches 39; Conservative (
                                                                                                                              97.3%;
97.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                    188 amino acids
                                                                                                                                             Best Local Similarity 97.59
Matches 39; Conservative
   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                  MOLECULE TYPE: protein US-08-801-863-3
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                                       amino acid
                                                            linear
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                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                              US-08-486-596A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                 LENGTH:
TYPE: ar
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STATE:
                                                                                                                            Query Match
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APPLICANT: Saha, Shankar
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 SFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146
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Pred. No. 1.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
APPLICANT: MATSOO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JO-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-070-504-15; Sequence 15, Application US/09070504; Patent No. 6268474; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.3%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-09-004-713-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 55401
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                  New York
                                                                                                                                                                                      USA
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                                                                                                                                                                                                         ZIP: 10020
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                                                                                                                                                                     STATE:
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; Sequence 3, Application US/09011922A; Patent No. 6320022; GENERAL INFORMATION.
; GENERAL INFORMATION:
APPLICANT: Cuttitta, Miller, Mae Jean; Unsworth, Edward APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward APPLICANT: As and Servi, Charles; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related; TITLE OF INVENTION: Product (PAMP) in Human Pathology and TITLE OF INVENTION: Physiology
; CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 31;
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100.0%; Pred. No. 5.6e-18;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA: 30-Aug-1995
PRIOR APPLICATION DATA: 10-Aug-1995
PRIOR APPLICATION DATA: 10-Aug-1996
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA: 1996
FILING DATE: 16-Aug-1996
          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: PreproAM(116-146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: MS WORD 97
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Best Local Similarity 100.0
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NY COUNTRY: USA ZIP: 10154-0053 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 31 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                              US-09-011-922A-3
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APPLICANT: Smith, Derek D.
APPLICANT: Shankar
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Mucting, Raasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 50;
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ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: Ploppy disk
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: MCCOTIMACK, MyTA H
REGISTRATION NUMBER: 180.00020101
TELECOMMUNICATION UNPBER: 180.00020101
TELECOMMUNICATION UNPBER: 180.00020101
TELECOMMUNICATION UNPSER: 180.00020101
TELECOMMUNICATION UNPSER: 180.00020101
TELECOMMUNICATION NUMBER: 180.00020101
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Best Local Similarity 100.0%; Pred. No. 5.6e-18;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      Score 196; DB 4;
Pred. No. 1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
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Patent No. 6268474
                                                                                                                         TELEFAX: 612/305-1228
INPOMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
                                                                                                                                                                                                                                                                                                                                                                                         89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 87.59
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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MOLECULE TYPE: peptide
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Gaps

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RESULT 13

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APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.0%; Score 57; DB 4; Length 13; 100.0%; Pred. No. 0.02;
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US-09-011-922A-2
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08966388
Patent No. 595412
GENERAL INTORMATION:
APPLICANT: Michla KUBOTA
APPLICANT: Michla KUBOTA
APPLICANT: Hiroto CHEN
APPLICANT: Toshio MIYAKE
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               Floppy Disk
                                                                                                                                                                                                                         345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-966-388-4
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              Sequence 14 Application US/09011922A

Sequence 14 Application US/09011922A

Sequence 14 Application US/09011922A

GENERAL INFORMATION:
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Marci, Charles
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue

CITY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic homolog of two-thirds of the intact AM peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.4%; Score 163; DB 4; L
100.0%; Pred. No. 5.6e-18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:

APPLICATION UNBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION NUMBER: US/60/013,172
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lessile A. Serunian
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 35,353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 759-480
TELEFHONE: (212) 751-6849
INFORMATION FOR SEQ. 1D NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/011,922A
FILING DATE: 17-FED-1998
FILING DATE: 17-FED-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TVQKLAHQIYQFTDKDKDKNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09011922A Patent No. 6320022 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
COTHER INFORMATION:
US-09-011-922A-14
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Best Local Similarity
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US-09-011-922A-2
        US-09-011-922A-14
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Gaps

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TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Mashington
STAFET: 0.3
COUNTRY: USA
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.7%; Score 52; DB 2; Length 775; 36.0%; Pred. No. 15; tive 7; Mismatches 9; Indels
                                                                                                                                                                                                                                              COMUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,388
FILING DATE:
CLASSIFICATION NUMBER: US/08/966,388
FILING DATE:
APPLICATION NUMBER: JP 311,235/1996
FILING DATE: 8-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 61,710/97
FILING DATE: 3-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INDRABR:
TELEFRAN: 202-628-5197
TELEFRAN: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:.
LENGTH: 775 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 36.05
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-966-388-4
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Search completed: October 17, 2002, 14:48:42 Job time : 5.49127 secs

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Gaps

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October 17, 2002, 14:45:20 ; Search time 12.5786 Seconds (without alignments) 459.181 Million cell updates/sec
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SIDSI/gcgdata/geneseqp/geneseqp-embl/AA1981.DAT:*

SIDSI/gcgdata/geneseqp/geneseqp-embl/AA1981.DAT:*

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SIDSI/gcgdata/geneseqp-embl/AA1999.DAT:*

SIDSI/gcgdata/geneseqpe-embl/AA1999.DAT:*

SIDSI/gcgdata/geneseqpe-embl/AA1999.DAT:*

SIDSI/gcgdata/geneseqpe-embl/AA1999.DAT:*

SIDSI/gcgdata/geneseqgp-embl/AA1999.DAT:*

SIDSI/gcgdata/geneseqgp-embl/AA1999.DAT:*

SIDSI/gcgdata/geneseqgp-embl/AA1999.DAT:*

SIDSI/gcgdata/geneseqgp-embl/AA1999.DAT:*

SIDSI/gcgdata/geneseqgp-embl/AA1999.DAT:*

SIDSI/gcgdata/geneseqgp-embl/AA1999.DAT:*
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1 YRQSMNNFQGLRSFGCRFGT......FTDKDKDNVAPRSKISPQGY
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                         US-10-018-924-2_COPY_95_146
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                             score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect :
                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results, predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	IIOTI TO CART	2 AAB75110 Human adrenomedull					22 AAB75113 Linker pentide-adr	AAB75122		AAB75124		
S Query Match Length DB		52	52	52	53	53	62				170	
& Query Match 1		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
Score	}	283	283	283	283	283	283	283	283	283	283	000
Result No.		Н	7	٣	4	2	9	7	ω	σ	10	,

Human adrenomedull	Porcine adrenomedu	Porcine adrenomedu			Rat adrenomedullin	Adrenomedullin pep					Adrenomedullin pep	Human adrenomedull	Adrenomedullin pep	Rat canalicular mu	Human cMOAT C-term	Multi-druq resista	Human canalicular	Human canalicular	Human preproadreno	Drosophila melanog	Mycobacterium auru	Mycobacterium auru	Drosophila melanog	S-Locus receptor (Brassica sp. S-rec	Drosophila melanog	Neisseria gonorrhe	Drosophila melanod	Arabidopsis thalia	Arabidopsis thalia	מ	ໝ	ß
2 AAB60344	22 AAB49698	2 AAB60345	2 AAE09819	AAB4969	_	2 AAB91765		:2 AAB91768	:2 AAB91761	-			2 AAB91760	.8 AAW33361	-	1 AAB28224					-	-		.5 AAR53404	-	-	-	2 ABB59224	_	1 AAG54151	1 AAG14117	-	1 AAG54149
	188 2																1545 1				339 2				828				82	82	٣	٣	
100.0	97.9	97.9	81.6	81.6			•	69.3	64.1		57.6	•	22.6	21.6	21.2	21.2	21.2	20.8	20.1	20.0	19.8	19.8	19.8	19.8	19.8	19.8	19.4	19.4	19.3	19.3	19.3	19.3	19,3
283	277	277	231	231	231	227	219.5	196	181.5	163	163	163	64	61	9	9	9	59	57	56.5	26	26	26	26	26	26	22	2	54.5		•	54.5	54.5
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                        Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                         Mitsushima K;
                                                                                                                                                                                                                                                                        Takimoto A, Mitsuda Y, Nakayama T,
                                                                                 Human adrenomedullin (AM) protein.
                      Ą.
                    AAB75110 standard; Protein; 52
                                                                                                                                                                                                                              99JP-0294147.
                                                                                                                                                                                                         10-OCT-2000; 2000WO-JP07023.
                                                              (first entry)
                                                                                                                                                                                                                                                    (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                              WPI; 2001-282044/29.
N-PSDB; AAH19806.
                                                                                                                                                             WO200127310-A1.
                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                             15-OCT-1999;
                                                                                                                                                                                   19-APR-2001.
                                                              31-JUL-2001
                                          AAB75110;
RESULT 1
          AAB75110
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Saha S,
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                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         US6268474-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1998;
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                                                                                                                                                                                                                                                                                                                     29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001.
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Best Local Simi
Matches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                           AAE09818;
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                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and malelmido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various discorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
                                   adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection, endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                        52
                                                                                                                                                                                     100.0%; Score 283; DB 22; Length 52; 100.0%; Pred. No. 2.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thibaudeau K;
                        invention describes a method (M1) for producing
                                                                                                                                                                                                                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                Adrenomedullin peptide (AM) SEQ ID NO:935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 498; 733pp; English.
 Disclosure; Page 45; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PG,
                                                                                                                                                                                                                                                                                                                                    Æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                   AAB91759 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2000; 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-112059/12.
                                                                                                                                                                                                  Local Similarity
                                                                                                                                                           52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-2000
                                                                                                                                                                                                               52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                             AAB91759
                                                                                                                                                            Sequence
                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                         RESULT 2
AAB91759
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Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
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1larity 100.0%; Pred. No. 2.6e-32;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                          100.0%; Score 283; DB 22; 100.0%; Pred. No. 2.6e-32;
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                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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10-OCT-2000; 2000WO-JP07023.
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               WO200127310-A1.
                                                                                                                                             L5-OCT-1999;
                                                                                                                                                                                                                                Takimoto A,
                                                        19-APR-2001
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                                                                                                                                                                                                                                Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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                                                                                                                                                                                       Glycine extended human adrenomedullin (AM-gly) protein.
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                                                          AAB75111 standard; Protein; 53 AA.
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nes 52; Conservative
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N-PSDB; AAH19807.
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Synthetic.
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Matches
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                                                                                                                                Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
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Nakayama T, Mitsushima K;
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100.0%; Pred. No. 2.7e-32;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                    Disclosure; Page 47; 75pp; Japanese.
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  Mitsuda Y,
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                                                       WPI; 2001-282044/29.
N-PSDB; AAH19808.
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Matches 52; Conserv
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Synthetic.
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exemplification of the present invention

120 AA;

Sequence

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                              Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a
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                                                                                             recombinant host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200127310-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                             Gaps
                                                                                                                                                                                                                                                                   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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                                                                     Length 120;
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                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
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Score 283; DB 22;
Pred. No. 7.1e-32;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitsushima
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100.0%; Pred. No. 7.1e-32;
live 0; Mismatches 0;
                                                                                                                                                                                                                                        UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakayama Т,
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                                                                                                                                                      AAB75123 standard; Protein; 120
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100.0%;
100.0%;
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                             Conservative
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Query Match
Best Local Similarity
Matches 52; Conserv
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les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 AA;
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RESULT 9

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(first entry)
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                                                                                                                                                                    Mitsuda Y,
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N-PSDB; AAF29138.
                                                                                                                                                                                                      WPI; 2001-282044/29.
N-PSDB; AAH19810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
52; Conserv
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                                                                                       15-0CT-1999;
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                                                                                                                                                                    Takimoto A,
              19-APR-2001
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Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
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                                                                                                                                                    Adrenomedullin, glycine extended adrenomedullin, AM, AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 283; DB 22;
100.0%; Pred. No. 9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitsushima
                                                                                                                 JspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thioredoxin-(GSGSGDAFE)-AM-gly protein.
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  AAB75124 standard; Protein; 147
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                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rakimoto A, Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-282044/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH19866
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                                                                                                                                                                                                               Homo sapiens.
Synthetic.
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                                                                           31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                            19-APR-2001
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                                    AAB75124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB73124 reperseent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                     rrouting adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 169
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                                                                                                                                                                                   Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 283; DB 22;
Pred. No. 1.1e-31;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adrenomedulin amino acid sequence.
                                                                                                                                                                                      Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 49-50; 75pp; Japanese.
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100.0%; Pr
tive 0;
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10-OCT-2000; 2000WO-JP07023.
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Gaps

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This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                 uropathic activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;
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                                                                                                                                                                                                                                                                                                           vesicle smooth muscle; uropathic acary disorder; incontinence; procine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 277; DB 22;
Pred. No. 8.4e-31;
0; Mismatches 1;
     Mismatches
                                                                                                                                                                                                                                                                         Porcine adrenomedulin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 31-33; 42pp; Japanese.
                                                                                                                                                               AAB49698 standard; Protein; 188 AA.
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98.1%;
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.1
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises adrenomedulin
                                                                                                                                                                                                                                                                                                                            adrenomedulin; urinary
                                                                                                                                                                                                                                                                                                               elongation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-080754/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAF29139
                                                                                                                                                                                                                                                                                                                                                                                                  WO200078338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1999;
                                                                                                                                                                                                                                       04-APR-2001
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
                                                                                                                                                                                                   AAB49698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB60345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
 Matches
                                                                                                                             RESULT 13
                                                                                                                                              AAB49698
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AAB60345
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                                         This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving uninary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence represents human adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for inhibiting automatic uterine contraction or contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                     Length 185;
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                                                                                                                                                                                                                                                                                                               1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                            100.0%; Score 283; DB 22; 100.0%; Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 283; DB 22;
Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                    Mismatches
     Claim 1; Page 26-27; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 37-38; 54pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB60344 standard; Protein; 185 AA
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-080755/09.
                                                                                                                                                                                                        185 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF27228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200078339-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanagita T;
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB60344;
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RESULT 12 AAB60344

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Gaps

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Indels

Length 188;

25

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calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intact cells either in vitro or in vivo to inhibit the effect of CGRP binding to its receptor. The present sequence is rat adrenomedullin peptide.
                  Vascactive peptides useful for inhibiting calcitonin gene related peptide receptor activity \boldsymbol{\cdot}
                                                                                           The invention relates to antagonists of the vasoactive peptide
                                                                                                                                                                                                                                                                                                                            Score 231; DB 22;
Pred. No. 5.1e-25;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: October 17, 2002, 14:47:59 Job time : 12.5786 secs
                                                                                                                                                                                                                                                                           81.6%;
84.6%;
                                                                 Claim 5; Column 25-26; 24pp;
                                                                                                                                                                                                                                                                                                        44; Conservative
WPI; 2001-564216/63
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                 50 AA;
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                                                                                                                                                                                                                                                                                                                                                                           inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence represents porcine adrenomedullin precursor.
                                                                                                                                                                                                                                                                                            Composition for inhibiting automatic uterine contraction or contraction
 uterine contraction inhibitor; premature birth; miscarriage; abortion; dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                               invention relates to a composition containing adrenomedullin for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; vasoactive peptide; calcitonin gene related peptide; CGRP; CGRP-receptor identification; adrenomedullin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 277; DB 22; Length 1 Pred. No. 8.4e-31; Indels n: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                         caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 43-44; 54pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.9%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE09819 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0070504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0070504
                                                                                                                                                     23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                           23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat adrenomedullin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                     WPI; 2001-080755/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 AA;
                                                                                                                                                                                                                                                                    N-PSDB; AAF27229
                                                                       WO200078339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001
                                                                                                  28-DEC-2000
                                                                                                                                                                                                                           Yanagita T;
                                              Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Best Local
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Gaps

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Length 50; Indels THIS PAGE BLANK (USSTO)

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 17, 2002, 14:45:20 ; Search time 5.96509 Seconds Run on:

(without alignments) 837.648 Million cell updates/sec

US-10-018-924-2_COPY_95_146

283 1 YRQSMNNFQGLRSFGCRFGT.....FTDKDKDNVAPRSKISPQGY Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dF			SUMMAKIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
7	283	100.0	185	7	JN0684	adrenomedullin pre
7	277	97.9		~	S41600	٠,
m	231	81.6		7	JN0766	adrenomedullin pre
4	65.5	23.1		~	JC1392	monophenol monooxy
2	61.5	21.7		~	T14536	S-locus-specific g
9	61	21.6		Н	S71839	
7	60.5	21.4	253	7	н81690	conserved hypothet
8	59	20.8		-	S71841	multidrug resistan
6	58.5	20.7		7	A99638	hypothetical prote
10	58.5	20.7		7	A85489	hypothetical prote
11	58.5	20.7		~	T14415	끙
12	57.5	20.3	429	ď	T07809	
13	57.5	20.3		~	AG2058	ABC transporter AT
14	57	20.1		7	PC4153	monophenol monooxy
15	56	19.8		~	T14529	S-locus-specific g
16	26	19.8		H	JQ1677	S-receptor kinase
17	55.5	19.6		7	G84107	lipopolysaccharide
18	2	19.6	46	7	T15540	hypothetical prote
19	52	19.4		~	S20799	hypothetical prote
20	S	19.4		Н	E69130	
21	54.5	19.3	6	7	E91004	hypothetical prote
22	•	19.3	6	N	E85637	
23	•	19.3	42	7	T07814	S-locus-specific q
24	•	19.3	43	~	A27827	S-locus-specific g
25	•	19.3	46	7	T46165	×
26	54	19.1	37	~	T05598	hypothetical prote
27	S	19.1	42	7	T14533	S-locus-specific g
28	53.5	18.9	107	7	H84839	late embryogenesis
29	ω,	18.9	35	7	H95398	probable ABC trans

F:147-185/Domain: carboxyl-terminal propertide *status predicted <CTP>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following F:110-115/Disulfide bonds: *status experimental F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

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Gaps

; 0

Query Match
100.0%; Score 283; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.7e-30;
Matches 52; Conservative 0; Mismatches 0; Indels

hypothetical prote S-locus specific g	S-locus-specific g hypothetical prote virulence-associat	protein T12C24.12 monophenol monooxy protein kinase C (protein kinase C (protein kinase C (protein kinase C (protein kinase C (protein kinase C (hypothetical prote	S-locus-specific g S-locus-specific g
B83963 T14424	T14423 T23197 C82867	G86259 YRHU1 KIHUCA	KIRTC KIMSCA KIRBC	KIBOC A37237 T21052	T14416 T14530
000	777	2		777	77
362	428 617 151	522 529 672	672 672 672	672 676 2374	428
18.9 18.9	18.9 18.9	18.7 18.7 18.7	18.7 18.7 18.7	18.7 18.7 18.7	18.6 18.6
53.5	53.5 53.5 53	ນ ເນ ເນ ເນ ເນ ເນ	23 23 33	23 23 33 33 33 33 33 33 33 33 33 33 33 3	52.5 52.5
30	3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	35 36 37	38 39 40	4 4 4 4 4 3 3 4 3	44 45

ALIGNMENTS

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Date: 03-Feb-1994 #sequence_revision 05-Feb-1994 #text_change 20-Jun-2000
C;Date: 03-Feb-1994 #sequence_revision 05-Feb-1994 #text_change 20-Jun-2000
C;Date: 03-Feb-1994 #sequence_revision 05-Feb-1994 #text_change 20-Jun-2000
A;Title: Genomic structure of human adrenomedullin gene.
A;Title: Cander 20-Feb-1994 #text_change 20-Jun-2000
A;Reference number: JC2351; MUD:9765329; PIDN:AAC660642.1; PID:9765330
A;Residues: 1-185 <1SH>
A;Coss-references: GB:S73906; NID:9765329; PIDN:AAC60642.1; PID:9765330
A;Rotoss-references: GB:S73906; NID:9765329; PIDN:AAC60642.1; PID:9765330
A;Reference number: JU; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Bjochem: Bjophys: Res. Commun. 194, 720-725, 1993
A;Title: Cloning and characterization of cDNA encoding a precursor for human adrenome A;Reference number: JN0684; MuID:93443928
A;Accession: JN0684; MuID:93443928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Mccesslou: FWD-190
A; Mccesslou: FWD-190
A; Residues: 22-41 <KII>
A; Residues: 22-41 <KII>
A; Residues: 22-41 <KII>
Biochem: Biophys. Res. Commun. 192, 553-560, 1993
A; Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A; Reference number: JN0476; MUID: 93249425
A; Residues: 95-146 <KII>
A; Molecule type: protein
A; Residues: 95-146 <KII>
A; Experimental source: pheochromocytoma
C; Genetics:
A; Gene: GDB: ADM
A; Cross-references: GDB: 217070; OMIM: 103275
A; Map position: 11pter-11qter
A; Introns: 33/2; 83/2
C; Keywords: amidated carboxyl end; blood pressure control; hormone
F; 1-21/Domain: signal sequence #status predicted <PEU>F; 22-41/Domain: signal sequence #status predicted <PEU>F; 22-41/Domain: proadrenomedullin #status predicted <PEU>F; 22-41/Domain: proadrenomedullin #status caperimental 
F; 22-41/Domain: proadrenomedullin #status experimental 
F; 22-41/Domain: proadrenomedullin #status experimental 
F; 22-41/Domain: proadrenomedullin #status predicted <PEU>F; 22-41/Domain: proadrenomedullin #status predicted <PEU>F; 22-41/Domain: proadrenomedullin #status experimental 
F; 22-41/Domain: proadrenomedullin #status experimental 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: mRNA
A; Residues: 1-185 < KIT>
A; Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A; Accession: PN0348
adrenomedullin precursor - human
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R;Takase, M.; Miura, I.; Nakata, A.; Takeuchi, T.; Nishioka, M.

Gene 121, 359-363, 1992

A;Title: Cloning and sequencing of the CDNA encoding tyrosinase of Japanese pond frog
A;Reference number: JC1392

A;Accession: JC1392

A;Molecule type: mRNA
A;Residues: 1-532 <TAKA
A;Residues: 1-532 <TAKA
A;Residues: DBJ:D12514; NID:9222946; PIDN:BAA02077.1; PID:9222947
R;Miura, I.; Okumoto, H.; Makino, K.; Nakata, A.; Nishioka, M.
Jpn. J. Genet. 70, 79-92, 1995
A;Title: Analysis of the tyrosinase gene of the Japanese pond frog, Rana nigromaculat
A;Reference number: I51169; MUID:95290234
A;Reference number: I51169; MUID:95290234
A;Reference number: L5170 MID:968/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-9, A',11-277 <MIU>A;Residues: 1-9, A',11-277 <MIU>A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: monophenol monooxygenase
C;Reywords: glycoprotein; oxidoreductase; transmembrane protein
F;47,90,115,165,234,294,341,360,375/Binding site: carbohydrate (Asn) (covalent) #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: 218078; MUID:97352858
A; Accession: T14536
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-430 < KUS>
A; Cross-references: EMBL:DB8212; NID:92351155; PIDN:BAA21946.1; PID:92351156
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TH4536
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14536
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o sechanism.
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Cispecles: Ratus norvegicus (Norway rat)
Cispecles: Ratus norvegicus (Norway rat)
Cispecles: 10-569-1999 #sequence_revision 10-5ep-1999 #text_change 19-Jan-2001
Cispecssion: 571839
Ribuechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; J. Biol. Chem. 271, 1501-15098, 1996
A; Title: CDNA cloning of the hepatocoyte canalicular isoform of the multidrug A; Reference number: 571839; MuID:96279006
A; Ratus: preliminary; nucleic acid sequence not shown
A; Status: preliminary; nucleic acid sequence not shown
A; Residues: 1-1541 < BUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 QSMNNFQGLRSFGCRFG----TCTVQK--LAHQIYQFTDKDKD-----NVAPRSKISP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.1%; Score 65.5; DB 2; Best Local Similarity 33.9%; Pred. No. 1.2; Matches 20; Conservative 8; Mismatches 18;
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A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: 22-41 <SA2>
C.Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom essure control.
C.Keywords: amidated carboxyl end
F.1-21/Domain: signal sequence #status predicted <SEG>
F.2-185/Product: proadrenomedullin #status predicted <PEU>
F.2-187/Product: proadrenomedullin #status predicted <AMT>
F.94-143/Product: adrenomedullin #status predicted <AMT>
F.94-143/Product: adrenomedullin #status predicted <AMT>
F.94-143/Product: adrenomedullin #status predicted <AMT>
F.94-143/Arodictided site: amidated carboxyl end (Arg) (amide in mature form from following gly F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl
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C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change ll-Jul-1997
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, Jo; Say. Res. Commun. 195, 931-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv A;Reference number: JN0766; MUID:93384621
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A;Reference number: S41600
A;Status: prellminary
A;Molecule type: mRNA
A;Residues: 1-188 <KIT>
A;Cross-references: GB:D14875; NID:9439721; PIDN:BAA03590.1; PID:9496379
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                                                                                                                                                                                                                                                                                                                     adrenomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S41600
R;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
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N;Alternate names: tyrosinase
C;Species: Rana nigromaculata (Japanese pond frog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: JC1392; ISI169
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                                                  YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
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Pred. No. 3.8e-23;
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Pred. No. 3e-29;
0; Mismatches
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1 Similarity 84.6%;
44; Conservative 3
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ilarity 98.1%;
Conservative
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A; Molecule type: mRNA
A; Residues: 1-185 <SAK>
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Best Local Similarity 37.8
Matches 14; Conservative
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Matches 11; Conserv
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A; Residues: 1-253 <TEF>
A; Experimental source: strain Nigg (MOPn)
A;Cross-references: EMBL:X96393; NID:g1292881; PIDN:CAA65257.1; PID:g1617207
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
C;Reywords: ATP; glycoprotein: nuclectide binding; P-loop; transmembrane protein
F;100-124/Domain: transmembrane #status predicted <TMO1>
F;127-151/Domain: transmembrane #status predicted <TMO2>
F;127-151/Domain: transmembrane #status predicted <TMO3>
F;305-329/Domain: transmembrane #status predicted <TMO5>
F;314-311/Domain: transmembrane #status predicted <TMO6>
F;354-381/Domain: transmembrane #status predicted <TMO6>
F;546/Domain: transmembrane #status predicted <TMO9>
F;556-564/Domain: transmembrane #status predicted <TMO9>
F;550-504/Domain: transmembrane #status predicted <TMO9>
F;560-674/Region: nucleotide-binding motif A (P-loop)
F;650-674/Region: nucleotide-binding motif A (P-loop)
F;1018-1046/Domain: transmembrane #status predicted <TMO1>
F;1018-1046/Domain: transmembrane #status predicted <TMO1+
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F;1313-1506/Domain: AFP-binding cassette homology <ABC2>
F;13130-1337/Region: nucleotide-binding motif A (P-loop)
F;6,1007,1010,1011/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: S71841; S71840
R;Kocaity, J; Kappler, D.
R;Kocaity, J; Kappler, D.
A;Reference number: S71841 Library, August 1996
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38.2%;
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Matches 13; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: TC0556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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A; Accession: S71841
A; Molecule type: mRNA
A; Residues: 1-1545 < KCDS>
A; Cross-references: EMBL:X96395; NID:g1507819; PIDN:CAA65259.1; PID:g1514568
A; Cross-references: EMBL:X96395; NID:g1507819; PIDN:CAA65259.1; PID:g1514568
B; Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler, J. Biol. Chem. 271, 15091-15098, 1996
A; Title: CDNA cloning of the hepatocyte canalicular isoform of the multidrug resistan A; Reference number: S71839; MUID:96279006
A; Title: CDNA cloning of the hepatocyte canalicular isoform of the multidrug resistan A; Reference number: S71839; MUID:96279006
A; Accession: S71840
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1415-1429, VP, 1432-1455, 'E', 1457-1545 < BUE>
C; Genetics: A; Cross-references: EMBL:X96395
C; Genetics: A; Gene: GDB:ABCC2; CMOAT; ABC; MRP2; CMRP; DJS
A; Cross-references: GDB:6089489; OMIM:601107
A; Map position: 10q24-10q24
C; Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology < ABC1>
C; Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology < ABC2>
F; 554-837/Domain: ATP-binding cassette homology < ABC2>
F; 1317-1510/Domain: ATP-binding cassette homology < ABC2>
F; 1334-1341/Region: nucleotide-binding motif A (P-100P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ECs0073 [imported] - Escherichia coli (strain O157:H7, substrain C:Species: Escherichia coli (species: IB-Jul-2001 #text_change 03-Aug-2001 (species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 (species: 10-120) (species: 10-120) (species: 11-22, 2001 species: 2001 spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 20078 [imported] - Escherichia coli (strain 0157:H7, substrain E C;Species: Escherichia coli Escherichia coli Escherichia coli Bistate: Id-Feb-2001 #text_change 14-Sep-2001 C;Accession: A895489 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001 A;Apitle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ
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C;Superfamily: Escherichia coli yabP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 KLAHQIYQFTD----KDKDNVAPRSKISPQG
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Thu Oct 17 15:36:27 2002

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17; Gaps

Indels

15;

------NVAPRSKISPOGY

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ABC transporter ATP-binding protein all2021 [imported] - Anabaena sp. (strain PCC 7120 K) whose: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C; Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C; Date: 14-Dec-2001 #text_change 11-Jan-2002 C; Accession: AG2058 R; Kaneko, T.; Nakamuta, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840 A; Cacession: AG2058 A; Accession: AG2058 A; Accession: AG2058 A; Accession: AG2058 A; Accession: AG2058 A; Caces-references: GB:BA000019; PIDN:BAB73720.1; PID:g1731112; GSPDB:GN00179 A; Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minophrenia monotygenase (EC. 114.10.1) CHILCKEN MINOPHRENIA MONOTYGENESE (EC. 114.10.1) CHILCKEN MINOPHRENIA MONOTYGENESE (EC. 114.10.1) CHILCKEN MINOPHRENIA GAILUS (CHICKEN)
C.Species: Gallus gallus (chicken)
C.Species: C.A.; Kidson, S.H.
Gene 169, 191-195, 1996
G. A.Title: Characteristic sequences in the promoter region of the chicken tyrosinase-en A; Reference number: PC4153; MUID:96194800
A; Reference number: PC4153; MUID:96194800
A; Residues: 1-273 <FER>
A; Residues: 1-273 <FER>
A; Residues: 1-273 <FER>
A; Residues: 1-273 <FER>
A; Rossicues: GB:L46805; NID:91146320; PIDN:AAB08441.1; PID:91146321
A; Note: The DNA sequence includes the first exon and a part of the first intron C; Comment: This enzyme is the rate-limiting enzyme in pigment blosynthesis.
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: monophenol monooxygenase
C; Keywords: oxidoreductase
                                                                                                 209 GLRSHRSGPWNGIRFSGIPEDQKSSYMVYSFTENSEEVAYTFRMTNSSIYSRLKISSEGF 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.1%; Score 57; DB 2; Length 273; 35.9%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
T14529
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 QGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 NFQGLRSFGCRFG----TCTVQKL--AHQIYQFTDKDKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monophenol monooxygenase (EC 1.14.18.1) - chicken
                                                                GLRSF - - - - - GCRF - GTCTVQKLAHQIYQFTDKDKD -
         10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 20.3%; Score 57.5;
Best Local Similarity 37.2%; Pred. No. 18;
Matches 16; Conservative 6; Mismatches
         Conservative
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         18;
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         Matches
                                                                                                                                                                                                                   RESULT 13
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                                                       A;Status: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-189 <STO>
A;Residues: 1-189 <STO>
A;Cross-references: GB:AE005174; NID:g12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP:20G
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gen
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C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: ATP; glycoprotein; magnesium; phosphotransferase; serine/threonine-specific
F;32-427/Domain: S-locus-specific glycoprotein homology <SSG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streceptor kinase (EC 2.7.1.-) - radish (fragment)
N.Alternate names: S glycoprotein
N.Alternate names: S glycoprotein
C.Species: Raphanus sativus (radish)
C.Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C.Accession: T07809
R.Sakamoto, K.; Kusaba, M.; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A.Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related g.A.Recession: T0780
A.Recession: T0780
A.Accession: T0780
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-429 <SAK>
A.Cross-references: EMBL:AB009677; NID:g3327839; PIDN:BAA31724.1; PID:g3327840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:D85215; NID:g2351161; PIDN:BAA21949.1; PID:g2351162
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-locus-specific glycoprotein - turnip (fragment)
N;Alternate names: S glycoprotein
C;Species: Barssica rapa (turnip)
C;bate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14415
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                    Length 189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                           Indels
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: A85489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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(7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58.5; DB Pred. No. 7.9; 8; Mismatches
                                                                                                                                                                                                                                                                                                                              Score 58.5; Di
Pred. No. 3.4;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57.5; |
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 KLAHQIYQFTD-----KDKDNVAPRSKISPQG 51
                                                                                                                                                                                                       C,Genetics:
A,Gene: 20078
C,Superfamily: Escherichia coli yabP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: 218078; MUID:97352858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
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1 Similarity 32.7%;
16; Conservative (
                                                                                                                                                                                                                                                                                                                           Query Match 20.7%;
Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
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Gaps

5

Indels

16;

Length 712;

DB 2;

18;

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Gaps

: 9

Indels

14;

39

Search completed: October 17, 2002, 14:46:18 Job time : 6.96509 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

October 17, 2002, 14:45:21; Search time 3.11222 Seconds Run on:

(without alignments) 646.939 Million cell updates/sec

US-10-018-924-2_COPY_95_146 Perfect score:

283 1 YRQSMNNFQGLRSFGCRFGT......FTDKDKDNVAPRSKISPQGY Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P35318 homo sapien	s sns	cani		P43145 rattus norv		Q04604 rana nigrom		Q08410 coturnix co		_				P14679 homo sapien	P04409 bos taurus		-	P10102 oryctolagus		P54834 canis famil	Q14314 homo sapien	006491 bacillus su	_	P07065 bacteriopha		_				P23073 simian foam	4	P05432 rattus norv
SUMMARIES	ID		ADML_PIG	ADML_CANFA	ADML_BOVIN	ADML_RAT	ADML_MOUSE	TYRO_RANNI	MRP2_RAT	TYRO_COTJA	MRP2_HUMAN	TYRO_CHICK	SYH_METTH	MRP2_RABIT	SLS6_BRAOL	TYRO_HUMAN	KPCA_BOVIN	KPCA_HUMAN	KPCA_MOUSE	KPCA_RABIT	KPCA_RAT	TYRO_CANFA	FGL2_HUMAN	GATA_BACSU	LIGD_PSEPA	TOP5_BPT4	VGLN_HUMAN	VG48_BPMU	TYRO_TRISI	MXID_SHIFL	MXID_SHISO	ENV_SFV1	MRP4_HUMAN	G33_RAT
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æ	Query Match	100.0	97.9	93.6	92.9	81.6	78.4	23.1	21.6	20.8	0	20.1	19.4	19.4	19.3	18.7	18.7	18.7	18.7	18.7	18.7	18.4	18.4	18.4	18.2	18.2	18.2	18.0	18.0	18.0	18.0	18.0	18.0	17.8
	Score	283	277	265	263	231	222	65.5	61	29	59	57	52	22	54.5	53	53	53	53	23	53	52	52	52	51.5	51.5	•	51	51	51	51	51	51	50.5
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347 drosophila	37 homo sapien	177 homo sapien	'd7 lactococcus	504 homo sapien	169 chlamydia m	ao chlamydia p	117 chlamydia t	245 mus musculu	889 homo sapien
P23647 P35736	P319	P304	Q9r7	566Ö	P568	5 26 0	0843	0622	8.00
FUSE_DROME	D3HI_HUMAN	1B35_HUMAN	GAL1_LACLA	EYA3_HUMAN	RPOB_CHLMU	RPOB_CHLPN	RPOB_CHLTR	SOS1_MOUSE	SOS1_HUMAN
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805 922.	336	362	399	573	1252	1252	1252	1319	1333
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50.5	50	20	20	20	20	20	20	20	20
34 35	36	38	39	40	41	42	43	44	45

ALIGNMENTS

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MEDLINE=20053666; PubMed=10588445;
Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
"Structure-activity relationships of adrenomedullin in the circulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and adrenal gland.";
Regul. Pept. 85:1-8(1999).
-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND YEATHER AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP
                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                        TISSUE=Pheochromocytoma;
MEDLINE=93343928; PubMed=7688224;
Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
"Cloning and characterization of cDNA encoding a precursor for human
                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsuc H., Eto T., "Adrenomedullin: a novel hypotensive peptide isolated from human pheochromocytoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S., Matsuo H., Eto T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Liver;
MEDLINE-94354869; PubMed-8074714;
MEDLINE-94354869; PubMed-8074714;
Mistamura T., Kojima M., Rangawa K., Hino J., Matsuoka H.,
Kitamura K., Eto T., Matsuo H.;
"Genomic structure of human adrenomedullin gene.";
Biochem. Biophys. Res. Commun. 203:631-639(1994).
                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 194:720-725(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 192:553-560(1993).
                                     185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Samson W.K.;
"Proadrenomedullin-derived peptides.";
Front. Neuroendocrinol. 19:100-127(1998).
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pheochromocytoma; MEDLINE=93249425; PubMed=8387282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98240137; PubMed=9578982;
                                   STANDARD;
                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 95-146.
                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 adrenomedullin.
                                 ADML_HUMAN
                                                                                                                                                                 ADM OR AM.
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RESULT 1
ADML_HUMAN
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AGENTS
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MOD_RES
SEQUENCE
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PROPEP
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                          SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
          PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIAND PITUITARY GLAND TO EXCLITARE THE LOSS OF PLASMA VOLUME, ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Adrenal medulla;
MEDLINE-9413945; PubMed-8043068;
Kitamura K., Kangawa R., Kojima M., Ichiki Y., Matsuo H., Eto T.;
"Complete amino acid sequence of porcine adrenomedullin and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION (G-42 PROVIDE AMIDE GROUP). AMIDATION (G-147 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM OR AM.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
                                                                                                                                                                                                                                                                                                                                                                                             Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YROSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION (G-147 PROVIDE A 64C7D2A0B4654DFE CRC64;
                                                                                                                                SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 283; DB 1;
100.0%; Pred. No. 1.3e-30;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA.
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
Hormone; Amidation; Cleavage on pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                          EMBL; S73906; AAC60642.1; -.
EMBL; D43639; BAA07756.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNA encoding its precursor.";
Lett. 338:306-310(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34, Created)
34, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20420 MW;
                                                                                                                                                                                                                                                               EMBL; D14874; BAA03589.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, 01-OCT-1996 (Rel. 34, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                 PIR; JN0476; JN0476.
PIR; JN0684; JN0684.
PIR; JC2351; JC2351.
MIM; 103275; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ma.
Local Sim.
52;
                                                                                                                    TISSUES
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P53366;
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MOD_RES
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PROPEP
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                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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077559; OGTVC9;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-2(
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
71749460F5660A61 CRC64;
                                                                                                                                                                                         -1 - FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hormone, Amidation, Cleavage on pair of basic residues, Signal. SIGNAL 1 \ 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó;
                                                                   Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
                                                                                        Kawamoto M., Minamino N., Matsuo H., Eto T.;
"Identification and hypotensive activity of proadrenomedullin
N-terminal 20 peptide (PAMP).";
FEBS Lett. 351:35-37(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREPROAM C-TERMINAL FRAGMENT (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Imoto I., Jougasaki M.;
"Cloning of cDNA encoding canine adrenomedullin.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                 KIDNEY.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted
SEQUENCE OF 22-41.
TISSUE-Adrenal medulla;
MEDLINE-94357274; PubMed-8076689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-99002704; Pubmed-9788655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D14875; BAA03590.1; -.
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Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .146
188
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DISULFID
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16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM): Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             its basal
 FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
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AMIDATION (G-147 PROVIDE AMIDE GROUP)
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                    AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
                                                                                                                                                                                                         Cleavage on pair of basic residues; Signal. 21 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barker-S., Wood E., Clark A.J.L., Corder R.;
"Cloning of bovine preproadrenomedullin and inhibition of its
expression in vascular endothelial cells by staurosporine.";
Life Sci. 62:1407-1415(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                 Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                             809D6A64F98F5578 CRC64;
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                                 SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                    Score 265; DB 1;
Pred. No. 3.4e-28;
                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
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0; Mismatches
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                                                                                                                                                                                                                                                                             SIMILARITY)
                                                                                                                                              EMBL; AF045773; AAD05423.1; -.
EMBL; U96127; AAD09957.1; -.
Interpro; IFR001710; Adrenomedullin.
Pfan; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
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                        Secreted
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MEDLINE=98244567; PubMed=9585168;
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                                                                                                                                                                                                                                                                                                                                                             20929 MW;
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94.2%;
                      SUBCELLULAR LOCATION:
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188
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                                                                                                                                                                                                          Hormone; Amidation;
                                                                                                                                                                                                                                                                                                                                                             188 AA;
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Molecular cloning and biological activities of rat adrenomedullin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION (G-147 PROVIDE AMIDE GROUP)
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                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                         Hormone, Amidation, Cleavage on pair of basic residues, Signal. SIGNAL
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Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
Matsuo H., Eto T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 YRQSLNNFQGLRSFGCRFGTCTVQKLAHQIYHFTDKDKDGSAPRSKISPQGY 146
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-:- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS,
HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
-:- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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Biochem. Biophys. Res. Commun. 195:921-927(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); P.
terminal peptide (ProAM-N20) (ProAM N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.9%; Score 263; DB 1;
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                                                                                                                                                                                                                                                                                            ADRENOMEDULLIN.
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                                                                                                                                                                                                                                                                   BY SIMILARITY
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                                                                                                                    EMBL, AJ001613; CAA04866.1; -.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
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MEDLINE=96102137; PubMed=8524787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Conservative
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16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                             PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yotsumoto S., Ko M.S.H.;
"Expression of mouse adrenomedullin gene in trophoblastic glant
"Expression of mouse adrenomedullin gene in trophoblastic glant
cells at the implantation site.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                             (BY SIMILARITY).
AMIDATION (G-144 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; "Genomic organization, expression, and chromosomal mapping of the
                                                                                                                                                                                          SIMILARITY).
BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                      Hormone, Amidation, Cleavage on pair of basic residues, Signal.
SIGNAL
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                        Length 185;
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                                                                                                                                                                                                                                                                                                               3; Indels
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SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                        Score 231; DB 1;
Pred. No. 1.2e-23;
                                                                                                                                                                    ADRENOMEDULLIN
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                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                        EMBL; D15069; BAA03665.1; -.
EMBL; U15419; AAB60519.1; -.
InterPro; IPR001710; Adrenomedullin.
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                                                                                            Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
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MEDLINE=97092892; Pubmed=8938454;
                                                                                                                                                                                                                                                      (BY
                                                                                                                                                                                                                                                                                                                                                                                                                   ADML_MOUSE STANDARD;
P97297; P97453;
16-OCT-2001 (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                     81.6%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse adrenomedullin gene. Genomics 37:395-399(1996).
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PROPEP
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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"Analysis of the tyrosinase gene of the Japanese pond frog, Rana nigromaculata: cloning and nuclectide sequence of the genomic DNA containing the tyrosinase gene and its flanking regions.";
Jpn. J. Genet. 70:79-82(1995).
-i- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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BY SIMILARITY.

AMIDATION (G-42 PROVIDE AMIDE GROUP)

(BY SIMILARITY).

AMIDATION (G-145 PROVIDE AMIDE GROUP)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                  Hormone, Amidation, Cleavage on pair of basic residues; Signal. SIGNAL 1 \\ 21 \\ \mathrm{BY} SIMILARITY.
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01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
TYR OR TYRS.
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MEDLINE-93077054; Pubmed-1446833;
Takase M., Miura I., Nakata A., Takeuchi T., Nishioka M.;
"Cloning and sequencing of the cDNA encoding tyrosinase of the
Japanese pond frog, Rana nigromaculata.";
Gene 121:359-363(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 184;
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Pred. No. 1.8e-22;
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C88C99045A79C898 CRC64;
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InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
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COFACTOR: BINDS TWO COPPER IONS.
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                                                                     EMBL; D78349; BAA11367.1;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Canalicular multispecific organic anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance
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MEDLINE-96180672; PubMed-8599091;
Paulusma C.C., Bosma P.J., Zaman G.J.R., Bakker C.T.M., Otter M.,
Scheffer G.L., Scheper R.J., Borst P., Oude Elferink R.P.J.;
"Congenital jaundice in rats with a mutation in a multidrug
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Pfam; PR064; tyrosinase; 1.
PRINTS; PR00092; TYROSINASE.
PROSITE; PS00497; TYROSINASE.1; 1.
PROSITE; PS00498; TYROSINASE.2; 1.
OXIGOTEGIUCTASE; MODIOXYGENASE, COPPET; Glycoprotein; Signal; Transmembrane; Melanin biosynthesis.
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COPPER A (BY SIMILARITY).
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MRP2_RAT
Signologo 063145;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seque)
1 15-JUL-1998 (Rel. 40, Last annot)
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STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-96279006; PubMed-8662992;
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ABCC2 OR CMOAT OR MRP2 OR CMRP.
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                                                                                                                     STRAIN=SPRAGUE-DAWLEY; TISSUE-Liver; Ito K., Stimizu T., Sugiyama Y.; Ito K., Suzuki H., Hirohashi T., Kume K., Shimizu T., Sugiyama Y.; Expression of the putative ATP-binding cassette region, homologous to that in multidrug resistance associated protein (MRP), is hereditarily defective in Elsai hyperbillirubinemic rats (EHBR)."; Int. Hepatol. Commun. 292.292-299 (1996).
i. FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMBROUS ORGANIC
                                                                                                                                                                                                                             ANIONS.
--- SUBCELLUAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
--- IDISEAGE: DEFECTS IN ABCC2 ARE A CAUSE OF HEREDITARY CONJUGATED HYPERBILIRUBINEMIA (EHBR).
--- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                            CDNA cloning of the hepatocyte canalicular isoform of the multidrug
Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
                                           resistance protein, cMrp, reveals a novel conjugate export pump deficient in hyperbilirubinemic mutant rats."; J. Biol. Chem. 271:15091-15098(1996).
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DOMAIN
1 26 EXTRACELLULAR (BY SIMILARITY).
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InterPro; IPR001140; ABC_transporter_tmem.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; APP_GTP_A.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
SMART; SM00382; AAA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93181407; PubMed=1292011;
MEDLINE-93181407; PubMed=1292011;
MEDLINE-93181407; PubMed=1292011;
MEDLINE-93181407; PubMed=1292011;
Tanaka S., Takeuchi S., Shibahara S., Takeuchi T.;
Phylogeny of regulatory regions of vertebrate tyrosinase genes.";
PHYLOGENY THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
COMPOUNDS. CAPALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO
INDOLE-5,6 QUINONE.

-I- CAPALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                              Gaps
                                            17 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

ATP (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

M-N WY (IN REF. 3).
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COFACTOR: BINDS TWO COPPER IONS.
SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00264; Tyrosinase.
Pfam; PF00264; Lyrosinase; 1.
PROSITE; PS00497; TYROSINASE_1; 1.
PROSITE; PS00498; TYROSINASE_1; 1.
Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal; Transmembrane; Melanin biosynthesis.
SIGNAL 19 277
                                                                                                                                                                                                                              Score 61; DB 1; Length 1541;
Pred. No. 4.8;
                                 EXTRACELLULAR (BY SIMILARITY).
 SIMILARITY).
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               SIMILARITY)
 CYTOPLASMIC (BY
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                                                                                                                                                                                                                                                                                                                                                                                                             273 AA
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                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                           18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 34, Created)
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38.2%;
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1007
1010
1011
420
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1251
1541
674
1337
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1541 AA;
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Matches 13; Conserv
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01-OCT-1996 (
01-NOV-1997 (
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Q08410;
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NP_BIND
CARBOHYD
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DOMAIN
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Kool M., de Haas M., Ponne N.J., Paulusma C.C., Oude-Elferink R.P.J.,
Baas F., Borst P.;
                                                                                                                                                                                                                Gaps
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Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
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                                                                                                                                                                                                                                                                                                                                                                 MRP2_HUMAN STANDARD; PRT; 1545 AA.
092887; 099663; 092798; 014022; 092500; 090MS2;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OUT-2001 (Rel. 40, Last annotation update)
Canalicular multispecific organic anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance
COPPER A (BY SIMILARITY).

COPPER A (BY SIMILARITY).

COPPER A (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98087571; PubMed-9425227;
Wada M., Toh S., Taniguchi K., Nakamura T., Uchiumi T., Kohno K.,
Yoshida I., Kimura A., Sakisaka S., Adachi Y., Kuwano M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'cDNA cloning of the hepatocyte canalicular isoform of the
                                                                                                                                                                            20.8%; Score 59; DB 1; Length 273; 35.9%; Pred. No. 1.5;
                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                              7 NFQGLRSFGCRFG----TCTVQKL--AHQIYQFTDKDKD 39
                                                                                                                                                                                              Pred. No. 1.5;
6; Mismatches
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nes 14; Conservative
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WEDLINE-99162196; PubMed-10053008;

Adachi Y., Sakisaka S., Kuwano M.;
To sakisaka S., Kuwano M.;
Transporter gene (MRP2/chOAT) and mutations in the ATP-binding-
transporter gene (MRP2/chOAT) and mutations in the ATP-binding-
Transporter gene (MRP2/chOAT)

Am. J. Hum. Genet. 64:739-746(1999).

C. !- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC

ANIONS. MAY FUNCTION AS A CELLULAR LOCATION: Integral membrane protein.

C. !- FUNCTION: MADIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC

ANIONS. MAY FUNCTION AS A CELLULAR LOCATION: Integral membrane protein.

C. !- FUNCTION: MADIATES HEPATOBILIARY EXPRESSED IN THE LIVER.

C. !- DISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF DUBIN-JOHNSON SYNDROME

COPROPORPHYRIN ISOMER I, DEPOSITION OF MELANIN-LIKE PIGMENT IN

C. !- PURPARILIE NORMAL LIVER FUNCTION.

C. !- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
  Mutations in the canilicular multispecific organic anion transporter
                     (cMOAT) gene, a novel ABC transporter, in patients with hyperbilirubinemia II/Dubin-Johnson syndrome."; Hum. Mol. Genet. 7:203-207(1998).
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InterPro; IPR001140; ABC_transporter_tmem.
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CAB45309.1;
CAB45309.1;
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AJ132310; CAB45309.1;
AJ132311; CAB45309.1;
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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CYTOPLASMIC (BY SIMILARITY).
B (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
9 (BY SIMILARITY).
10 (BY SIMILARITY).
11 (BY SIMILARITY).
12 (BY SIMILARITY).
13 (BY SIMILARITY).
14 (BY SIMILARITY).
15 (BY SIMILARITY).
16 (BY SIMILARITY).
17 (BY SIMILARITY).
18 (BY SIMILARITY).
19 (BY SIMILARITY).
11 (BY SIMILARITY).
11 (BY SIMILARITY).
12 (BY SIMILARITY).
13 (BY SIMILARITY).
14 (BY SIMILARITY).
                                                                                                                                                                2 (BY SIMILARITY).

EXTRACELULAR (BY SIMILARITY).

3 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

4 (BY SIMILARITY).

5 (BY SIMILARITY).

5 (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
15 (BY SIMILARITY).
15 (BY SIMILARITY).
16 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; APP_GTP_A.
Pfam; PF000664; ABC_tran; 2.
Pfam; PF00005; ABC_tran; 2.
SMARY; SM0382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
                                                                                                                    EXTRACELLULAR (BY SIMILARITY).

1 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1545;
                                                                                                                                                                                                                                                                                           6 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
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Q -> R (IN DJS).

/FTIG=VAR_010756.

V -> E (IN REF. 2).

V -> G (IN REF. 5).

C -> Y (IN REF. 2).

MW; EA12668A4DD0F391 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 50
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Pred. No. 8.9;
5; Mismatches
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Best Local Similarity 37.8%;
Matches 14; Conservative
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1515 151
1545 AA;
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                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).

COPPER A (BY SIMILARITY).

COPPER A (BY SIMILARITY).

COPPER B (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                 Mochii M., Tio A., Yamamoto H., Takeuchi T., Eguchi G.; "Isolation and characterization of a chicken tyrosinase cDNA."; Pigment Cell Res. 5:162-167(1992).
                                                                                                                                                                                                                     "Characteristic sequences in the promoter region of the chicken tyrosinase-encoding gene."; Gene 169:191-195(1996).
                                                                                                                                                                                                                                                                                                                                        -1- COFACTOR: BINDS TWO COPPER IONS.
-1- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
-1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal; Transmembrane; Melanin blosynthesis.
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EMBL; L46805; AAB08441.1; --
InterPro; IPR00227; Tyrosinase.
Pfam; PF00264; tyrosinase.
PRINTS; PR00092; TYROSINASE.
PROSITE; PS00497; TYROSINASE.1; I.
PROSITE; PS00498; TYROSINASE.2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       blosynthesis
                                                                                           SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN;
MEDLINE-93157254; Fubbmed-1494538;
                                                                                                                                                                                   SEQUENCE OF 1-273 FROM N.A. MEDLINE-96194800; Pubmed-8647445;
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Best Local Similarity 35.9%;
Matches 14; Conservative 5
                                                                                                                                                                                                        Ferguson C.A., Kidson S.H.;
                        Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371
529 AA;
                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
CARBOHYD
CARBOHYD
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Gaps

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14; Indels

Pred. No. 5.4; 5; Mismatches

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PROSITE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
Aminoacyl-trnA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee H.-M., Dubois J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Kagale P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                 Methanobacterium thermoautotrophicum.
Archaea, Euryarchaeota, Methanobacteriales, Methanobacteriaceae;
                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
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425 AA
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Interpro; IPR002106; AA_tRNA_ligase_II.
Interpro; IPR004154; HGTP_anticodon.
Interpro; IPR002314; tRNA-synt_2b.
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                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03129; HGTP anticodon;
Pfam; PF00587; tRNA-synt_2b; 1
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                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=145262
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SEQUENCE 425 AA
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Q28689;
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026346;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                                                                                                                                                                          chloride

    I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
    I- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SWALL

30-MXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Canalicular multispecific organic anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance protein) (Epithelial basolateral chloride conductance regulator).
ABCC2 OR MRP2 OR EBCR.
                                                                                                                                                                 van Kuijck M.A., van Aubel R.A.M.H., Busch A.E., Lang F., Russel F.G.M., Bindels R.J.M., van Os C.H., Deen P.M.T.; Molecular cloning and expression of a cyclic AMP-activated chloric conductance regulator: a novel ATP-binding cassette transporter."; Proc. Natl. Acad. Sci. U.S.A. 93:5401-5406(1996).
                                                                                                                                                                                                                                             MEDLINE-98279125; PubMed-9614209;
van Aubel R.A.M.H., van Kuijck M.A., Koenderink J.B., Deen P.M.T.,
van Os C.H., Russel F.G.M.;
                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
                                                                                                                                                                                                                                                                              Adenosine triphosphate-dependent transport of anionic conjugates
                                                                                                                                                                                                                                                                                           the rabbit multidrug resistance-associated protein Mrp2 expressed
                                                                         Oryccolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
5 (BY SIMILARITY).
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7 (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
9 (BY SIMILARITY).
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InterPro; IPR001687; ATP_A.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
SMARY; SM00382; AAA; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                               Pharmacol. 53:1062-1067(1998)
                                                                                                                                                       MEDLINE-96224297; PubMed-8643587;
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                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                            NCBI_TaxID=9986;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Nature 326:523-523(1987).
-!- FUNCATION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
(THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
-!- TISSUE SPECIFICITY: STTCAMA.
-!- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.; "Amino-acid sequence of glycoproteins encoded by three alleles of the S locus of Brassica oleracea."; Nature 326:617-619(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica oleracea (Cauliflower).

Bukaryota, Viidiplantae; Streeptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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"A cDNA clone encoding an S-locus-specific glycoprotein from Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      INKED (GLCNAC. . .) (POTENTIAL).
D8FBF5AC8FE45873 CRC64;
                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                    EXTRACELLULAR (BY SIMILARITY).
11 (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
13 (BY SIMILARITY).
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15 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
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  CYTOPLASMIC (BY SIMILARITY)
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16-OCT-2001 (Rel. 40, Last annotation update)
S-locus-specific glycoprotein S6 precursor (SLSG-6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55;
Pred. No.
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P07761;
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Bouchard B.,
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 There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                    S-LOCUS-SPECIFIC GLYCOPROTEIN S6.
N-LINKED (GLCNAC. .) (POTENTIAL).
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MEDLINE-88041128; PubMed=2823263;
Kwon B.S., Haq A.K., Pomerantz S.H., Halaban R.;
Isolation and sequence of a cDNA clone for human tyrosinase that maps at the mouse c-albino locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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P14679; Q15676; Q15675; Q15680;
01-APR-1990 (Rel. 14, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
(Tumor rejection antigen AB) (SK29-AB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.3%; Score 54.5; DB 1; Length 436; 28.6%; Pred. No. 9.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 52
                                                                                                                                                                                                                                                          Polymorphism; Signal.
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Proc. Natl. Acad. Sci. U.S.A. 85:6352-6352(1988)
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the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
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                                                                                                                        PIR; A27827; A27827.
InterPro; IPR001480; B_lectin.
InterPro; IPR003609; Pan_app.
InterPro; IRR000858; Slocus_91ycop.
                                                                                                            EMBL; X03170; CAA26934.1; ALT_INIT
                                                                                                                                                                                       Pfam; PF01453; Agglutinin; 1.
Pfam; PF00954; S.locus glycop; 1.
SWART; SW00108; B_lectin; 1.
SWART; SW00473; PAN_AP; 1.
Self-incompatibility; Glycoproteir
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TISSUE-Melanoma;
MEDLINE-89279151; Pubmed-2499655;
                                                                                                                                                                                                                                                                                                                                                                                                                   49779 MW;
                                                                                             EMBL; Y00268; CAA68375.1;
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436 AA;
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Oetting W.S., King R.A.; "Molecular basis of type I (tyrosinase-related) oculocutaneous albinism: mutations and polymorphisms of the human tyrosinase gene."; Hum. Mutat. 2:1-6(1993).
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                                                                                           SEQUENCE FROM N.A. MEDDMed=1711223; MEDLINE=91271371; PubMed=1711223; Chintamaneni C.D., Halaban R., Kobayashi Y., Witkop C.J., Kwon B.S.; and single base insertion in the putative transmembrane domain of the tyrosinase gene as a cause for tyrosinase-negative oculocutaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;
MEDLINE-90089403; PubMed-2480811;
KIKUChi H., Miura H., Yamamoto H., Takeuchi T., Dei T., Watanabe M.;
"Characteristic sequences in the upstream region of the human tyrosinase gene.";
Biochim. Biophys. Acta 1009:283-286(1989).
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Giebel L.B., Strunk K.M., King R.A., Hanifin J.M., Spritz R.A.;
"A frequent tyrosinase gene mutation in classic, tyrosinase-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,
                                                                                                                                                                                                                                                            TISSUE-Melanoma, and T-cell;
MEDLINE-33440625; PubMed-8340755;
Brichard V., van Woelfel T., Woelfel C., de Plaen E.,
Lethe B., Coulie P., Boon T.;
"The tyrosinase gene codes for an antigen recognized by autologous cytolytic T lymphocytes on HLA-A2 melanomas.";
J. EXP. Med. 1781489-495(1993).
Souchard B., Fuller B.B., Vijayasaradhi S., Houghton A.N.;
Induction of pigmentation in mouse fibroblasts by expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                King R.A., Spritz R.A.;
"Tyrosinase gene mutations associated with type IB ('yellow') oculocutaneous albinism.";
[14]
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MEDLINE-90259036; PubMed=2342539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of albinism: mutations and polymorphisms pigmentation genes associated with albinism."; Hum. Mutat. 13:99-115(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (type IA) oculocutaneous albinism.";
Proc. Natl. Acad. Sci. U.S.A. 87:3255-3258(1990)
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New Engl. J. Med. 322:1724-1728(1990).
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MEDLINE=93237884; PubMed=8477259;
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                                        human tyrosinase cDNA.";
J. Exp. Med. 169:2029-2042(1989).
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"Mutations of the tyrosinase gene in Indo-Pakistani patients with type
I (tyrosinase-deficient) oculocutaneous albinism (OCA).";
Am. J. Hum. Genet. 53:1173-1179(1993).
                                                                                                                                                                                                                                                                                                                                                   VARIANT OCA-ITS GLN-422.
MEDLINE-91154384; PubMed=1900309;
Giebel L.B., Tripathi R.K., King R.A., Spritz R.A.;
"A tyrosinase gene missense mutation in temperature-sensitive type I oculocutaneous albinism. A human homologue to the Siamese cat and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breimer L.H., Winder A.F., Jay B., Jay M.; "Initiation codon mutation of the tyrosinase gene as a cause of human albinism.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Octting W.S., King R.A.; "Molecular analysis of type I-A (tyrosinase negative) oculocutaneous
                                                                                                                            Tripathi R.K., Strunk K.M., Glebel L.B., Weleber R.G., Spritz R.A.; "Tyrosinase gene mutations in type I (tyrosinase-deficient) oculocutaneous albinism define two clusters of missense substitutions.";
Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.
King R.A., Spritz R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94070862; PubMed-7902671;
Tripathi R.K., Bundey S., Musarella M.A., Droetto S., Strunk K.M.,
Holmes S.A., Spritz R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gershoni-Baruch R., Rosenmann A., Droetto S., Holmes S., Tripathi R.K., Spritz R.A.; "Mutations of the tyrosinase gene in patients with oculocutaneous albinism from various ethnic groups in Israel."; Am. J. Hum. Genet. 54:586-594(1994).
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MEDLINE-96243675; PubMed-8644824;
Summers C.G., Octting W.S., King R.A.;
"Diagnosis of coulocutaneous albinism with molecular analysis.";
Am. J. Ophthalmol. 121:724-726(1996).
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"Non-random distribution of missense mutations within the human
tyrosinase gene in type I (tyrosinase-related) oculocutaneous
                                                                                                                                                                                                                                               MEDLINE-91118940; PubMed-1899321; Spritz R.A., Strunk K.M., Hsieh C.-L., Sekhon G.S., Francke U.; Homozygous tyrosinase gene mutation in an American black with tyrosinase-negative (type IA) oculocutaneous albinism."; Am. J. Hum. Genet. 48:318-324(1991).
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MEDLINE-95043421; PubMed=7955413;
                                                                            VARIANTS OCA-IA SER-21; TRP-217; HIS-299; SER-403; SER-446 AND
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                                             J. Hum. Genet. 49:696-696(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Invest. 87:1119-1122(1991).
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MEDLINE~94175072; PubMed=8128955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Chim. Acta 227:17-22(1994).
                                                                                                ASN-448.
MEDLINE-92351982; PubMed-1642278;
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Hum. Mol. Genet. 6:659-664(1997).
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Spritz R.A., Oh J., Fukai K., Holmes S.A., Ho L., Chitayat D.,
France T.D., Musarella M.A., Orlow S.J., Schnur R.E., Weleber R.G.,
                                           Morell R., Spritz R.A., Ho L., Pierpont J., Guo W., Friedman T.B.,
Asher J.H. Jr.,
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19;
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                                                                                                                                                                                                                                                                                                                                    "Novel mitations of the tyrosinase (TVR) gene in type I oculocutaneous albinism (OCA1).";
Hum. Mutat. 10:171-174(1997).
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Pred. No. 1
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                        MEDLINE=97301760; PubMed=9158138;
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30.2%;
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Matches 13; Conservative
VARIANT GLN-402
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 17, 2002, 15:20:12; Search time 9.48534 Seconds (without alignments) 742.931 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-018-924-2_COPY_4_185 947 1 VSVALMYLGSLAFLGADTAR.....SKPQAHGAPAPPSGSAPHFL 182

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	CI		ADML_PIG	ADML_BOVIN	ADML_CANFA	ADML_RAT	ADML_MOUSE	TTP_HUMAN	FA5_HUMAN	CEFD_STRCL	A2AA_MOUSE	DNAA_STRCO	MPI2_RAT	A2AA_RAT	TBR1_HUMAN	REPA_AGRTU	YNE1_CAEEL	TTP_RAT	A2AA_HUMAN	KR1_HSV2H	VP40_SCMVC	YRF1_YEAST	CYAA_PODAN	GAG_SIVAT	T2D5_MOUSE	YRF4_YEAST	YRF2_YEAST	YRF3_YEAST	YRF6_YEAST	PTRR_MOUSE	T2D5_RAT	A2AA_PIG	TBR1_MOUSE	ICPO_PRVIF
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APC_MOUSE TTP_MOUSE ELKI_MOUSE PIRR_RAT ICPO_HSV2H ICRO_HSV2H ICRO_LSV2H TTP_BOUIN CBX8_HUMAN PRGR_HUMAN BRAC_BRARE CCAG_RAT
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ALIGNMENTS

RESULT ADML_H	RESULT 1 ADML_HUMAN							
ᄗ	ADML_HUMAN	STANDARD;	RD;	PRT;	185	AA.		
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E 5	01-FEB-1994	(Rel. 28,	Created)	£	1	;		
5 E		(Kel. 28,	Last st	eduence	updat	(e)		
E	ADM precurson	r (Contai	ns: Adre	nomedu]	lin	AM);	Proadrenomedullin	edullin N-20
日日	terminal peptide (ProAM-N20) (ProAM N-terminal	tide (Pro	AM-N20)	(Proam	N-ter	minal		20 peptide) (PAMP)].
GN	ADM OR AM.							
SO	Homo sapiens (Human)	(Human)						
ر ت	Eukaryota; Metazoa;	etazoa; C	Chordata;	Crania	ta;	/ertek	Craniata; Vertebrata; Euteleostomi;	leostomi;
ပ္ပ	Mammalia; Eu	theria; F	rimates;	Catarı	hini,	HOM	Catarrhini; Hominidae; Homo.	ċ
ŏä	NCBI_TaxID=9606;	606;						
3 9	(T)	5						
η υ Γ	TISSUENCE FROM N.A	M N.A.						
2 X	MEDLINE=93343928: PubMed=7688224;	3928: Pub	Med=7688	3224:				
RA	Kitamura K.,	Sakata J	., Kanga	wa K.	Kojin	na M.,		, Eto T.;
RT	"Cloning and characterization of cDNA encoding	characte	rization	of cD	lA end	coding		
RT	adrenomedullin.";	in.";				,		
RL	Biochem. Biophys. Res. Commun. 194:720-725(1993)	phys. Res	. Commur	1. 194:7	20-73	25(199)	3).	
RN N	[2]							
КЪ	SEQUENCE FROM N.A	M N.A.						
R C	TISSUE=Liver;							
×	MEDLINE=94354869; PubMed=8074714;	4869; Pub	Med=807	1714;				
RA	Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka	, Kojima	M., Kang	yawa K.,	Hinc	, . L o	Ή	
RA	Kitamura K.,	Eto T.,	Matsuo 1	·: ·			,	
RT		structure of human adrenomedullin gene.";	human s	drenome	dull	ın ger		
Z:	chem.	phys. Res	. Commui	. 203:(31-6	39(195	4).	
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RP.	SEQUENCE OF	95-146.						
۲ پ	TISSUE=Pheochromocytoma;	hromocytc	ma;					
¥ 6	WEULINE=93249425; FullMed=838/262;	3423; FUL	Med=636	202;	-	1 1 1 1	Malan	
A G	Mitamura K., Kangawa K., Kawamoto M.,	kangawa +o m	K., Kawa	AMOCO M	, IC	TCUIKI	I., Nakamura	٠.٠
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X	MEDI, INE=98240137: PhhMed=9578982:	0137: Pub	Med=9578	3982:				
RA.	Samson W. K.		3					
. E	"Proadrenomedullin-derived peptides.";	dullin-de	rived pe	eptides				
R.	Front. Neuro	endocrino	1. 19:10	0-127(998)			
N.	[5]							
RP.	REVIEW.							
ž	MEDLINE=20053666; PubMed=10588445;	3666; Put	Med=105	38445;				
ΚĀ	Champion H.C., Nussdorfer G.G., Kadowitz P.J.;	., Nussdc	orfer G.(3., Kado	witz	P.J.,		
RŢ	"Structure-a	ctivity r	elation	ships of	adre	enome	lullin in th	he circulatio
RT	and adrenal	gland.";						
RL	Regul. Pept.	85:1-8(1	. (666					
ပ္ပ	- i - FUNCTION	: AM AND	PAMP AR	E POTENT	HYP(CLENS	VE AND VASC	ODILATATOR
ပ္ပ	AGENTS.	AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST	ACTIONS	HAVE BI	EN R	EPORTI	ID MOST RELA	RELATED TO THE
ပ္ပ	PHYSIOLO	GIC CONTF	OL OF F	CUID AND	ELE	CIROL	PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS	ASIS. IN THE
ပ္ပ	KIDNEY,	AM IS DIU	RETIC A	ND NATR	URET	IC, A	KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP	AND PAMP

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INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN PRIJUTARY GLAND, BOTH PRETIDES AT PHYSICLOGICALLY RELEVANT DOSES INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN AND PITUTARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME. ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
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ADM precursor [contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
ADM OR AM:
                                                                                                           TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
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AMIDATION (G-147 PROVIDE AMIDE GROUP).
64C7D2A0B4654DFE CRC64;
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                                                                                                                         ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
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                                                                                                                                                        SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 947; DB 1;
Pred. No. 7.7e-78;
Mismatches 0;
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                                                                                           SUBCELLULAR LOCATION: Secreted
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EMBL; D43639; BAA07756.1; ALT_SEQ.
PIR; JN0476; JN0476.
PIR; JN0684; JN0684.
PIR; JC2351; JC2351.
MIN; 103275; -
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                                                                                                                                                                                                                                                                                                                                                                  -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123
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                                                                    TISSUB-Adrenal medulla; MEDLINE-94139945; PubMed-8043068; Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.; "Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encoding its precursor."; FEBS Lett. 338:306-310(1994).
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AMIDATION (G-42 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
71749460F5660A61 CRC64;
                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
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   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 IYQFTDKDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRIWTS; PR00801; ADRENOMEDULN.
Hormone; Amidation; Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                     Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y., Kawamoto M., Minamino N., Matsuo H., Eto T.; "Identification and hypotensive activity of proadrenomedullin N-terminal 20 peptide (PAMP)."; FEBS Lett. 351:35-37(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.3%; Score 817; DB 1; Le
89:1%; Pred. No. 3.2e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
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                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                         TISSUE-Adrenal medulla;
MEDLINE-94357274; PubMed-8076689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEAL_BOVIN STANDARD;
062827;
16-0CT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D14875; BAA03590.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
146
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                          SEQUENCE OF 22-41.
                               NCBI_TaxID=9823;
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45
95
153
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146
                                                                                                                                                                                                                                                                                                                                      AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                  KIDNEY
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MOD_RES
SEQUENCE
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ADML_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
E SE
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NCBI_TaxID=9615;
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                                                                                                                                                                                                         AGENTS
                                                                                                                                                                                                                                                                                                                                                               InterPro;
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MOD_RES
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ID ADMI
AC P431
DT 01-N
DT 01-N
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                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADML_CANFA STANDARD; PRT; 188 AA.
077559; 09TVC9;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
                                                                                                                                                                                                                                                                                                                                                                                                      PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VPVALMYLGSLAFLGVDTARLDVAABFRKKWNKWALSRGKRELRESSSYPTGLADVKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                    in and inhibition of its basal
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-2
                                                       Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (b) SMALLARKITI).
AMIDATION (G-147 PROVIDE AMIDE GROUP)
(BY SIMILARTY).
(3002E79AB3B6612C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY.
BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                     EMBL; AJ001613; CAA04866.1; -.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; Diar of basic residues; Signal,
Hormone; Amidation; Cleavage on pair of basic residues; Signal,
21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 IYHFTDKDKDGSAPRSKISPQGYGRRRRRSLPEAGLGRTLLQPPEPKLRGAP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 774.5; DB 1; Length 188; Pred. No. 2e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVS-SKPQAHGAP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Indels
                                                                                                                                                                                                            CIRCULATION CONTROL (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY. ADRENOMEDULLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2e-6
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                 TISSUE=Aorta;
MEDLINE-98244567; PubMed=9585168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
87.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AA;
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                  NCBI_TaxID=9913;
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148
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MOD_RES
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ono Y., Kojima M., Okada K., Kangawa K.;
"CDNA Cloning of canine adrenomedullin and its gene expression in the
heart and blood vessels in endotoxin shock.";
shock 10:243-247(1958).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION (G-147 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
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                                                                                            Eukaryota; Metazoà; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Indels
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Indoto I., Jougasaki M.;
"Cloning of CDRA encoding canine adrenomedullin.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> K (IN REF. 2).
809D6A64F98F5578 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;; Score 771; DB 1;
;; Pred. No. 4.2e-62;
10; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99002704; PubMed=9788655;
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PRINTS; PR00801; ADRENOMEDULN.
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20929 MW;
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92
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188 AA;
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1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
AGENTS
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                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                        MEDLINE=96102137; PubMed=8524787; White R.F., Clark R.K., Willette R.N., Wang X., Yue T.L., Barone F.C., White R.F., Feuerstein G.Z.; Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.; Discovery of adrenomedulin in rat ischemic cortex and evidence for its role in exacerbating focal brain ischemic damage."; Proc. Natl. Acad. Sci. U.S.A. 93:11480-11484(1995).
                                                                                                                                                                                     MEDLINE-93384621; PubMed-7690563; Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K., Amatsuo H., Eto T.; Matsuo H., Eto T.; Molecular cloning and biological activities of rat adrenomedullin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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BY SIMILARITY.
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                   Proadrenomedullin N-20
 16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-2(
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION (G-144 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUNG, KIDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
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SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.-1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                          ochem. Biophys. Res. Commun. 195:921-927(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.9%; Score 624.5; DB 1
72.0%; Pred. No. 5.1e-49;
Live 14; Mismatches 32
                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-Adrenal gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
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InterPro, IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
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                                                                      Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                            hypotensive peptide.
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149
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                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
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Best Local Simi
Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGENTS
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PROPEP
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                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells at the implantation site.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (G-145 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                              Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; "Genomic organization, expression, and chromosomal mapping of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yotsumoto S., Ko M.S.H.; "Expression of mouse adrenomedullin gene in trophoblastic glant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cleavage on pair of basic residues; Signal. 21 BY SIMILARITY.
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InterPro; IPR001710; Adrenomedullin.
Pfam: PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97092892; PubMed-8938454;
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ADML_MOUSE STANDARD; F P97297; P97453; I6-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequin-corr-2001 (Rel. 40, Last annotation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse adrenomedullin gene.";
Genomics 37:395-399(1996).
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nes 119; Conserv
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STANDARD;
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                                                             LAHQIYQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edgington T.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphocytes."
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                                                                                                                                                                                          FA5_HUMAN
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                                                            117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   æ
                                  61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                       64 TOTLDPFLDEQNTTGPLQASNQSEAHIRVKRYRQSMN--QGSRSNGCRFGTCTFQKLAHQ 121
             63
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDILNB-91288233; PubMed=2062660;
Taylor G.A., Lai W.S., Oakey R.J., Seldin M.F., Shows T.B.,
Eddy R.L. T., Blackshear P.J.;
Eddy R.L. Tr., Blackshear P.J.;
and chromosomal localization of the mouse and human genes.";
Nucleic Acids Res. 19:3454-3454(1991).
I-FUNCTION: PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER
STRUCTURE INVOLVED IN REGULATORY PROTEIN WITH A NOVEL ZINC FINGER
STRUCTURE INVOLVED IN REGULATING THE RESPONSE TO GROWTH FACTORS.
HAS BEEN EXPERIMENTALY SHOWN TO BE ABLE TO BIND ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- MKGASRSPE 78
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Tristerraproline (TTP) (TISIIA protein) (TISI) (ZFP-36) (Growth factor-inducible nuclear protein NUP475) (GO/GI switch regulatory
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein; Repeat; Metal-binding; Zinc-finger; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAP 173
                                                                                            122 IYQLTDKDKDKDGMAPRNKISPQGYGRRRRRSLLEVLRSRTVESSQEQTHTAPAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDD9AD950AF7AF98 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89.5; DB Pred. No. 0.61;
                                                                                                                                                                    326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
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C3H1-TYPE 2.
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p-p-p-6.
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                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                   protein 24).
ZFP36 OR TIS11A OR TTP OR G0S24
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                                                                                                                                                                   STANDARD;
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128
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MIM; 190700; -.
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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219
109
147
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ZN_FING
SEQUENCE
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"Posttranslational sulfation of factor V is required for efficient thrombin cleavage and activation and for full procoagulant activity."; Biochemistry 33:6952-6959(1994).
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                                               -OK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-87260886; PubMed-3110773;
Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., Aldape R.A.,
Hewick R.W., Kaufman R.J., Mann K.G.;
"Complete cDNA and derived amino acid sequence of human factor V.";
                                                                                                                                                         ---FTDKDKDNVAP-----RSKISPOGYGRRRRSLPEAGPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kane W.H., Davie E.W.;
"Cloning of a cDNA coding for human factor V, a blood coagulation factor homologous to factor VIII and ceruloplasmin.";
Proc. Natl. Acad. Sci. U.S.A. 83:6800-6804(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P12259; Q14285;
01-0CT-1989 (Rel. 12, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Coagulation factor V precursor (Activated protein C cofactor).
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MEDLINE=93203619; PubMed=8454869;
Shen N.L.L., Fan S.-T., Pyati J., Graff R., Lapolla R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pittman D.D., Tomkinson K.N., Michnick D., Selighsohn U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-22232668; Pubmed=1567832;
Cripe L.D., Woore K.D., Kane W.H.;
"Structure of the gene for human coagulation factor V.";
Biochemistry 31:3777-3785(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 84:4846-4850(1987).
DSSPDAARIRVKRYRQSMNNFQGLRSFG----CRFGT-CTV-
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                                                                                                                                                                                                                                                                                                       159 TLVSSKPQAHGAPAPPSGSAP 179
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Query Match
Best Local Similarity
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PDB; 1
PDB; 1
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                                                                                                                                                                                                          activated protein C.";
Nature 369:64-67(1994).
-I-FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
-I-SUBUNIT: Factor Va is composed of a heavy chain and a light chain, noncovalently bound. The interaction between the two chains is calclum-dependent.
-DOMAIN: DOMAIN B CONTAINS 35 X 9 AA TANDEM REPEATS, AND 2 X 17 AA REPEATS.
                                                                                                                                                                                                                                                                                                            Thrombin activates factor V proteolytically to the active cofactor, factor Va (formation of a heavy chain at the N-terminus and a light chain at the C-terminus).

FTM. SULFATION IS REQUIRED FOR EFFICIENT THROMEIN CLEAVAGE AND ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY.

DISEASE: OWNERN PARABEMOPHILLA, AN HEWORRHAGIC DIASTESIS, IS DUE TO A DEFICIENCY OF FACTOR V. OTHER DEFECTS IN FS RESULTS IN A FORM OF THROMBOPHILLA KNOWN AS APC RESISTANCE (APCR). THE APCR MUTATION IS FOUND IN ABOUT 5% OF THE POPULATION WHICH SUGGEST THAT IMPLANTATION.
                                                                                                                                                                      MEDLINE-94217810; PubMed-8164741;
Bertlan R.M., Koeleman B.P.C., Koster T., Rosendaal F.R.,
Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.;
"Mutation in blood coagulation factor V associated with resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF 2 PLASTOCYANIN-LIKE REPEATS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
                                                            X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 2065-2224.
MEDLINE-20052169; PubMed-10586886;
Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A., Kim S.W.,
Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T., Kane W.H.,
                                                                                                                  'Crystal structures of the membrane-binding C2 domain of human
                     Hortin G.L.; "Sulfation of tyrosine residues in coagulation factor V."; Blood 76:946-952(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOINED JOINED
           MEDLINE-90366699; PubMed-2168225;
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AAB59401.1;
AAB59401.1;
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L32755; AAB59401.1;
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AAB59401.1;
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AAB59401.1;
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                                                                                                                                                            VARIANT APCR GLN-534.
                                                                                                                             coagulation factor V
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L32760;
                                                                                                         Fuentes-Prior
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InterPro; IPR001117; Cu-oxidase.
InterPro; IPR00421; FA58_C.
Pfam; PP00394; Cu-oxidase; 3.
Pfam; PF00754; F5_F8_type_C; 2.
SNART; SM00231; FA58C; 2.
PROSITE; PS010879; MULTICOPPER_OXIDASE1; 2.
PROSITE; PS01286; FA58C_1; 2.
PROSITE; PS01286; FA58C_1; 2.
Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen; Repeat; Polymorphism; Disease mutation; Thrombophilia; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO 14 AA REPEATS IN BOVINE FAS.
35 X 9 AA APPROXIMATE TANDEM REPEATS OF
[TNP]-L-S-P-D-L-S-Q-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEAVY CHAIN. ACTIVATION PEPTIDE (CONNECTING
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PLASTOCYANIN-LIKE 2.
F5/8 TYPE A 2.
PLASTOCYANIN-LIKE 3.
PLASTOCYANIN-LIKE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COAGULATION FACTOR V.
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EMBL, L32774; AAB59401.1; JC
EMBL; L32775; AAB59401.1; JG
EMBL; L32777; AAB59401.1; JG
EMBL; L32777; AAB59401.1; JG
EMBL; L32778; AAB59401.1; JC
EMBL; M16967; AAB59401.1; JC
EMBL; M16967; AAB59532.1; --
PIR; A28897; A28897.
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1CZT; 26-NOV-99.
1CZV; 26-NOV-99.
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SIGNAL 1 28
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FLDLDLSRIP-CDFYAGSGHKWLLA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                173 PPSGSA 178
                                                                                                                                                                                                               340 PPGTDA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS
                                                                                                                                                                                                                                                                                             A2AA_MOUSE
Q01338;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                 847 IRLLSLGAGEFKSQEHAKHKGPKVERDQAAKHRFSWMKLLAHKVGRHLSQDTGSPSGMRP 906
   Gaps
                                  3 VALMYLGSLAFLGADTAR-----LDVASEFRKKWNKWALSRGKRELRMSSSYPTGLAD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: BIOSYNTHESIS OF CEPHALOSPORIN ANTIBIOTICS. SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIINE-90299822; PubMed-1694525;

Kovacevic S., Tobin M.B., Miller J.R.;

"The beta-lactam biosynthesis genes for isopenicillin N epimerase adacetoxycephalosporin C synthetase are expressed from a single transcript in Streptomyces clavuligerus.";

J. Bacteriol. 172:3952-3958(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=1901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                  56 VKAGPAQTLIRPQDMKGASRSPED----SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Purification and properties of isopenicillin N epimerase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3%; Score 88.5; DB 1; Length 397;
24.7%; Pred. No. 0.94;
tive 20; Mismatches 63; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces clavuligerus.";
Biochim. Biophys. Acta 999:78-85(1989).
--- FUNCTION: CATALYZES THE REVERSIBLE ISOMERIZATION BETWEEN
ISOPERICILLIN AND PERICILLIN N.
--- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                   907 WEDLPSODTGSPSRMRPWKDPPSDLLLLKQSNSSKILVGRWHLAS------
                                                                                                                                                                  CTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYGRRRRSLPEAG-PGR 158
                                                                                                                                                                                       EMBL; M32324; AAA26714.1; -.
InterPro; IPR00192; Aminotransf_class_V.
Pfam; PF00266; aminotram.5; 1.
PROSITE; PS00595; AA_TRAA_FRR_CIASS_5; 1.
Antibiotic biosynthesis; Isomerase; Pyridoxal phosphate.
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 216 PYRIDOXAL PHOSPHATE (BY S 397 AA; 43366 MW; A152741899F192FF CRC64;
   71;
                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
1010penicillin N epimerase (EC 5....).
                                                                                                                                                                                                                                                                                   397 AA
     Mismatches
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-23.
MEDLINE-90028393; PubMed-2804141;
Usui S., Yu C.-A.;
   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces clavuligerus
     Conservative
                                                                                                                                                                                                                                                                                     STANDARD;
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     39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-9234211; Pubmed-1353249;
MEDLINE-9234211; Pubmed-1353249;
Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
"Cloning of two mouse genes encoding alpha 2-adrenergic receptor subtypes and identification of a single amino acid in the mouse alpha 2-c10 homolog responsible for an interspecies variation in antagonist binding.";
                                                                                                                                                                                                             125 TDKDKDNVAPRSKISPQGYGRRRRSLPEAG-----PGRTLVS-SKPQAHGAPA--- 172
                                                                                                                                                                                                                                                               --PTGVGFLHLAPGRLEELEPTQVS 243
                                                                                    GASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT-----CTVQKLAHQIYQF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOI. Pharmacol. 42:16-27(1992).-i- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                         244 WAYEPPEGSGPPAARDR-----FGSTPGLRRLECE-GTRDICPWLATPESIDFQ----
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PRINTS; PRO0021; 7tm_1; 1.

PRINTS; PRO00237; GPRRHODDPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50263; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; G-protein coupled receptor; Transmembrane; Glycoprotein; G-frome family; Phosphorylation; Lipoprotein; Palmitat.

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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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WGD; MGISH934; Adra2a.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.
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01-APR-1993 (Rel. 25, Last sequ
16-OCT-2001 (Rel. 40, Last anno
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TRANSMEM
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STRAIN-NRK49F;
MEDLINE-94208523; PubMed-8156993;
                                                            EMBL; AF187159; AAA26734.1; -. EMBL; AL357152; CAB92999.1; -.
                                                                                                             InterPro; IPR003593; AAA.
InterPro; IPR001957; Bac_DnaA.
Pfam; PP00308; bac_dnaA; 1.
PRINTS; PR00051; DNAA.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                        Local Similarity 25.4 ies 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                PIR; A41870; A41870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                               173 EKKGAGGGOOPAEPSCKINDOKWYVIS-----SSIGSFFAPCLIMILVYVRIYQIA-K 224
                                                                                                                                                                                                                                                                                                                                                                                                                                  128 DKDNVAPRSK----ISPQGYGRRRRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calcutt M.J., Schmidt F.J.; "Conserved gene arrangement in the origin region of the Streptomyces coelicolor chromosome.";
                                                                                                                                                                                        IMPLICATED IN CATECHOL AGONIST BINDING
                                                                                                                                                                                                          (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                      BY SIMILARITY.
PALMITATE (BY SIMILARITY).
IMPLICATED IN LIGAND BINDING (BY
                                                                                                                                                                                                                                                                                                  DB 1; Length 450;
                                                                                                                                                                                                                                                                                                                                    54; Indels
                   6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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F07E225393AFA93B CRC64;
     CYTOPLASMIC (POTENTIAL).
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Chromosomal replication initiator protein dnaA.
DNAA OR SCHIB.16C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            656 AA.
                                                                                                                                                                                                                                                                                                                  14; Pred. No. 1.5;
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                                                                                                                                                                            SIMILARITY).
                                                                                                                                                                                                                                                                                                  Score 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 174:3220-3226(1992).
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 374
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SEQUENCE FROM N.A.
 218
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                                                                  DOMAIN
CARBOHYD
CARBOHYD
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entities requires a license agreement (See http://www.lsb-s1b.ch/announce/or send an email to license@lsb-s1b.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 SRSPEDSSPDAARIRVK-RYRQS--MNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 PAGPAPQAPQSPPSRPQHRYEEPELPAPGQGGRE------EYRDRDE- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 LGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphatase functioning early in the cell cycle.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine + phosphate.
ENZYME REGULATION: STIMULATED BY CYCLINS B.
SIMILARITY: STRONG, TO OTHER SPECIES M-PHASE INDUCER PHOSPHATASE
AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES.
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PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cd625A is a novel phosphatase functioning early in the cell cycle.
EMBO J. 13:1549-1556(1994).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCED.
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Okayama H.;
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
M-phase inducer phosphatase 2 (EC 3.1.3.48) (Dual specificity phosphatase Cdc25B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.2%; Score 87; DB 1; Length 656; 25.4%; Pred. No. 2.3; 1.1ve 16; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 NVAPRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 ----YEGYGRNRADQLPTARP-----AYPQEYQRPEPGSWPRP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01008; DNAA; 1.
DNA replication; DNA-binding; ATP-binding.
NP_BIND 357 364 ATP (POTENTIAL).
SEQUENCE 656 AA; 73182 MW; 6C1D5C0193D3C92B CRC64;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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445
450 AA;
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                                                                                                                                                                                                                                                                                                                                                                        106
                                                                                                                                                                                                                                                                                                                                                                                                               114 PSPMDPQTAERTFEQAIQAASRVIQKMQFTIKASVFASEAAGHSPVLQNITNSQALDSW- 172
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FUNCTION: ALPHA-2 ADRENBRGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISP-----QGYGRRRRSLPEAGPGRTL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wypijewski K., Duda T., Sharma R.K.;
"Structural, genetic and pharmacological identity of the rat alpha
"Structural, genetic and pharmacological its molecular
2-adrenergic receptor subtype cA2-47 and its molecular
characterization in rat adrenal, adrenocortical carcinoma and bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lanier S.M., Downing S., Duzic E., Homcy C.J.;
Isolation of rat genomic clones encoding subtypes of the alpha 2-
adrenergic receptor. Identification of a unique receptor subtype.";
J. Biol. Chem. 266:10470-10478(1991).
                                                                                                                                                                                                                                                                                               6 MYLGSLAFLGADTARLDVAS-EFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-ARP-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2ARR)
(CA2-47) (Alpha-2D adrenergic receptor).
                                                                                                                                                                                                                                                                                                                                                                          ----YROSMNNFOGLRSFG
                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                  8.8%; Score 83.5; DB 1; Length 574; 23.3%; Pred. No. 4; Live 23; Mismatches 79; Indels 53
                                                                                                                                                              BY SIMILARITY.
9367CE203B15FAAD CRC64;
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                                                                                                                                       Cell division; Mitosis; Hydrolase; Multigene family.
ACT_SITE 481 481 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 AA.
                                                                                                                                                                                                                                                                                                                                                                          65 IRPQDMKGASRSPEDSSPDAARIRVKR-----
                        4SSP; P30305; 10B0.
InterPro; IPR000751; MPI_Phosphatase.
InterPro; IPR001763; Rhodanese_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-91125329; PubMed-2177834;
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MEDLINE-95349560; PubMed~7623790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 VSSKPQAHGAPAPPSGSAPHFL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 AEWASRREAFTQRPS-SAPDLM 232
                                                                                                                                                                            574 AA; 64286 MW;
                                                                               Pfam; PF00581; Rhodanese; 1.
PRINTS; PR00716; MPIPHPHTASE.
SMART; SM00450; RHOD; 1.
      EMBL; D16237; BAA03762.1;
                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                       1 Similarity
47; Conserv
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P22909;
                                                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                             Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 DKDNVAPRSK----ISPQGYGRRRRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 EKKGAGGGQQPAEPSCKINDQKWYVIS-----SSIGSFFAPCLIMILVYVRIYQIA-K 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPLICATED IN CATECHOL AGONIST BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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IMPLICATED IN LIGAND BINDING (BY
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GL -> AV (IN REF. 1).

A -> G (IN REF. 2).

RP -> PR (IN REF. 1).

P -> R (IN REF. 1).

D -> N (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
PALMITATE (BY
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                                                                                                                                                                         EMBL; M62372; AAA42034.1; -.
EMBL; U79031; AAC24959.1; -.
PIR; B40392; B40392.
HSPR; J4190; J410190.
HSSP; P29274; 1MMH.
GCRDb; GCR_0154; -.
GCRDb; GCR_0200; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 SDTDNFP-------DSKDSPGDVQRSKLSPVLDGVSELRHSFDGSAADR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 KRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNF 99
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuron 15:63-78(1995).
-1- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
DEVELOPMENTAL PROCESSES. TBR1 IS REQUIRED FOR NORMAL BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95344783; PubMed-7619531; Bulfone A., Smiga S.M., Shimamura K., Peterson A., Puelles L., Rubenstein J.L.R.; T. Prain-1: a homolog of Brachyury whose expression defines molecularly distinct domains within the cerebral cortex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 682;
                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
T-brain-1 protein (T-box brain protein 1) (TBR-1) (TES-56).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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PROSITE; PS01264; TBOX_2; 1.
PROSITE; PS50252; TBOX_3; 1.
Transcription regulation; DNN-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573 POLY-ALA.
74053 MW; E1C8D84206EFBBB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: BRAIN.
-!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
                                                                                           682 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
8.5%; Score 80.5; Di
Best Local Similarity 23.9%; Pred. No. 9;
Matches 34; Conservative 18; Mismatches
                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 TLVSSKPQAHGAPAPPSGSAPH 180
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MIM; 604616;
InterPro; IPR001699; T-box.
                                                                                        STANDARD;
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PRINTS; PR00937; TBOX.
SMART; SM00425; TBOX; 1.
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682 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           rissue-Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                   TBR1_HUMAN
Q16650;
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RESULT 15 REPA_AGRIU

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 VKAGPAQTL-IRPQDMKG----ASRSPEDSSPDAARIR-----VKRYRQSMNNFQGLR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 E-----TVEDRTRABQLAGYVER----AAQNRPSGPRKAARRRQQSRCSFTTPNR-PRR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 KORLPLEPAGARPRALLGKYVRKAAPLPD----DAAQARQERHDTIKAHMDSLSPADRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYGRRRRS----LPEAGPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Minimal region necessary for autonomous replication of pTAR."; J. Bacteriol. 170:3170-3176(1988).
                                                                                                                                                                                                                                              Plasmid pTAR.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 27.2%; Pred. No. 3.2;
Matches 52; Conservative 24; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A43662; A43662.
Plasmid; DNA replication.
SEQUENCE 250 AA; 27987 MW; CCED106534831979 CRC64;
                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
   250 AA.
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Job time : 11.4853 secs
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-88257036; Pubmed-3290199;
Gallie D.R., Kado C.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M21299; AAD15307.1; -.
                                                                                                                                                                                                                    Agrobacterium tumefaciens
STANDARD;
                                                                                                                                                                                                                                                                                                            Rhizobiaceae; Rhizobium
NCBI_TaxID=358;
                                                                                                                                                         Replicating protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPY NUMBER.
REPA_AGRTU
P15394;
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4

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 17, 2002, 15:20:13 ; Search time 17.1922 Seconds (without alignments) 1017.222 Million cell updates/sec Run on:

US-10-018-924-2_COPY_4_185 947 1 VSVALMYLGSLAFLGADTAR......SKPQAHGAPAPPSGSAPHFL 182 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1: * 2: pir2: * 3: pir3: * 4: pir4: * PIR_71:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	adrenomedullin pre		DI	ъ	\neg		isopenicillin N ep	alpha-2 adrenergic	dnaA protein - Štr	Id		ved	alpha-2-adrenergic	protein F56B3.4 [1	alpha-2-adrenergic	replicating protei	hypothetical prote	epithelial microtu	TIS11 protein - ra	probable inositol	alpha-2A-adrenergi	protein kinase (EC			probable membrane	adenvlate cyclase	gag polyprotein -	transcription fact	O.
SUMMARIES	QI .	JN0684	S41600	JN0766				_			T29586							S24457							S28368		JC4747		JC424	-
	DB	:						7																						
	Query Match Length	185	188	185	1116	326	2224	398	450	656	260	574	1051	450	926	450	250	458	749	320	383	450	481	1196	1224	1796	2145	519	678	199
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hypothetical prote protein Y57G11C.9	hypothetical prote polynucleotide pho hypothetical prote	hypothetical prote probable membrane probable membrane	parathyroid hormon conserved hypothet protein F55A8.1 (i	hypothetical prote alpha-2-adrenergic hypothetical Brach	hypothetical prote transcription regu
T27245 H88904	T27246 AC1241 S70310	S59693 S63325 S64633	S44203 T35971 E88640	T02286 A38316 I78558	T21052 AG3448
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553 568	659 723 1382	1681 1859 1859	591 860 294	327 450 681	2374 327
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77.5	77.5	77.5	77 77 76.5	76.5 76.5 76.5	76.5
30 31	32 34 34	35 36 37	38 39 40	41 42 43	44

ALIGNMENTS

	RESULT 1 JN0684
	adrenomedullin precursor - human
	c;petcter; none saptens (man) C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text change 20-Inn-2000
	R.Ishlmitsu, T.; Kojima, M.; Knangawa, K.; Hino, T.; Matsuoka, H.; Kitamura, K.; Eto, Riochem Biochem Biochem 203 631-639
	Aritle: Genomic structure of human adrenomedulin gene.
	A:Reference number: JC2351; MUID:94354869
	A A A Cocession: 1 CZ 351
	A. Notecute Cype: DAA A. Residues: 1-185 <ish></ish>
	A;Cross-references: GB:S73906; NID:q765329; PIDN:AAC60642.1; PID:q765330
	A. Experimental source: pheochromocytoma
	R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
	Biochem Biophys Res. Commun. 194, 720-725, 1993
	A)Tille: Cloning and characterization of CDNA encoding a precursor for human adrenome
	A.Accession: JN0684 MOIDS 3545920
	A:MOJECULE TYDE: MRNA
	A; Residues: 1-185 <kit></kit>
	A;Cross-references: GB:D14874; NID:9455470; PIDN:BAA03589.1; PID:9500612
	A; Accession: PN0548
	A; Molecule type: protein
	A; Residues: 22-41 <ki2></ki2>
	R;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
	Blochem. Blophys. Res. Commun. 192, 553-560, 1993
	Afille: Adrenomedulin: A novel novel nypovensive peptide isolated from numan pheochromocy a seference number: INDA76. MITD:030404036
	A. Accession: JN0476
_	A; Molecule type: protein
_	A; Residues: 95-146 <ki3></ki3>
	A; Experimental source: pheochromocytoma
_	C; Genetics:
	A;Gene: GDB:ADM
_	A;Cross-references: GDB:217070; OMIM:103275
	A;Map position: 11pter-11qter
	A; Introns: 33/2; 83/2
	C; Keywords: amidated carboxyl end; blood pressure control; hormone
	F.17-21-Dulalli . Signal sequence *Status predicted <2515. F.22-185/Product. nroadrenomedullin #status nroadioted <0815.
	F.22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <pap></pap>
	F;95-146/Product: adrenomedullin #status experimental AMAT>
	F;147-185/Domain: carboxyl-terminal propeptide #status predicted <ctp></ctp>
	F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
	Fill-115/Disulfide bonds: #status experimental
	F/140/MOGIIIEG SILE: AMIDATEG CALDOXYI ENG ($1/YF$) (AMIDE IN MATURE FORM FOULDWING

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Gaps

0;

Ouery Match 100.0%; Score 947; DB 2; Length 185; Best Local Similarity 100.0%; Pred. No. 5.2e-80; Matches 182; Conservative 0; Mismatches 0; Indels (

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F:94-143/Product: adrenomedullin #status predicted <MAT>
F:41/Modified site: amidated carboxyl end (Arg) (amide in m F:143/Modified site: amidated carboxyl end (Tyr) (amide in
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Best Local Similarity 22.2 Matches 36; Conservative
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C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change ll-Jul-1997
C;Accession: Junof65; PN0610
R;Sakata, J: Shimokubo, T.; Kitamura, K; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T Biochem. Blophys. Res. Commun. 195, 291-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv A;Reference number: Junof66; MuID:9384621
A;Accession: Junof66
A;Molecule type: mRNA
A;Residues: 1-185 cSAK>
A;Accession: PN0610
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 22-41 cSAZ>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenomedsule control.
C;Reywords: amidated carboxyl end
E;1-21/Domain: signal sequence #status predicted <SIG>F;22-185/Product: proadrenomedullin #status predicted <PBD>F;22-185/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAD>F;22-41/Product: proadrenomedullin amino-terminal 20 peptide
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                                                                                                                                                                                       61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                  121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPHAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
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                                       VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
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89.1%; Pred. No. 5.1e-68;
ive 10; Mismatches 9; Indels
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Matches 156; Conservative
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A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1116 <WUX>
A; Residues: 1-1116 <WUX>
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A; Residues: 21/1; 85/1; 175/3; 217/1; 361/3; 697/3; 891/1; 1008/1; 1072/1
mature form from following mature form from following
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16112
R;Wu, X.
Submitted to the EMBL Data Library, November 1995
     in mature form from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
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                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VSIALMLIGSLAVLGADTARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVP 63
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                                                                                                                                                                                                                                                                                                                                                                                                             1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                  'n
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                                                                                                                                                                            Length 185;
                                                                                                                                                                      Query Match 65.9%; Score 624.5; DB 2; Length Best Local Similarity 72.0%; Pred. No. 2.8e-50; Matches 126; Conservative 14; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 I----SPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 FGVTLAAPKGFGSISSLTEKPSSSIKSFGSWKPSSRSSPAPP 230
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C;Gonment: Factor V is activated by infombin and partially by congulation factor V is activated by infombin and partially by congulation factor V is activated by infombin and partially by congulation factors. F58671; 58871; A;Map position: 1q23-1q23
A;Introns: 53/2; 84/1; 125/1; 196/1; 244/1; 318/1; 373/2; 432/3; 466/1; 537/3; 588/1; A;Introns: 53/2; 84/1; 125/1; 196/1; 244/1; 318/1; 373/2; 432/3; 466/1; 537/3; 588/1; A;Pathway: blood coaqulation factor V; discoidin I amino-terminal homology; ferroxidase C;Reywords: blood coaqulation factor V stratus predicted cAMP: F129-137/Product: coaqulation factor V #stratus predicted cAMP: F129-33/Pomain: signal sequence fastats predicted cAMP: F129-33/Pomain: ferroxidase repeat homology cF01>
F139-33/Domain: ferroxidase repeat homology cF02>
F139-33/Domain: ferroxidase repeat homology cF02>
F135-40/Domain: ferroxidase repeat homology cF02>
F136-11/100/Domain: ferroxidase repeat homology cF03>
F137-120/Domain: ferroxidase repeat homology cF03>
F137-120/Domain: ferroxidase repeat homology cF03>
F136-11/100/Domain: ferro
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Comment: Factor V is activated by thrombin and partially by coagulation factor Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 VKAGPAQTLIRPQDMKGASRSPED----SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VALMYLGSLAFLGADTAR-----LDVASEFRKKWNKWALSRGKRELRMSSSYPTGLAD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 2224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 CTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAG-PGR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| :::| | | |:| | | ||:| | | ||:| | | ||:| | | ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    907 WEDLPSODTGSPSRMRPWKDPPSDLLLLKOSNSSKILVGRWHLAS---
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.4%; Score 89; DB 23.2%; Pred. No. 10; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: 226033; MŪID:90299822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 23.23
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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C;Species: Homo saplens (man)
C;Date: 19-Way 1989 sequence_trevision 02-Jun-1995 #text_change 08-Dec-2000
C;Accession: A65172; A42344; A20028; A2498; A25897
R;Cripe. LD.; Moore, X.D.; Kane, W.H.,
Biochemistry 31, 3777-3785, 1992
A;Fitle: Structure of the gene for human coagulation factor V.
A;Reference number: A42344; MUID:92220568
A;Residues: 1-222 4-CRIP
A;Residues: 1-222 4-CRIP
A;Residues: 46-58;79-89;120-130;191-201;239-249;313-323;368-378;428-437;461-471;533-542;
A;Residues: 46-58;79-89;7211-210;2172-318;-CRIP
A;Residues: 46-58;79-89;7211-210;2172-318;-CRIP
A;Residues: 46-58;79-89;7211-210;2172-318;-CRIP
A;Residues: 46-58;79-89;78-89;78-864, FR, 866-924, FE, 926-1763; T', 1765-2212, T', 2214-2224 4-JENN
A;Residues: 1-657, FR, 859-864, FR, 866-924, FE, 926-1763; T', 1765-2212, T', 2214-2224 4-JENN
A;Residues: 1-657, FR, 899-864, FR, 866-924, FE, 926-1763; T', 1765-2212, T', 2214-2224 4-JENN
A;Residues: 1-657, FR, 899-864, FR, 866-924, FE, 926-1763; T', 1765-2212, T', 2214-2224 4-JENN
A;Residues: 1-657, FR, 899-864, FR, 866-924, FE, 926-1763; T', 1765-2212, T', 2214-2224 4-JENN
A;Residues: 1-657, FR, 899-864, FR, 866-924, FE, 926-1763; T', 1765-2212, T', 2214-2224 4-JENN
A;Residues: 1-657, FR, 899-864, FR, 866-924, FE, 926-1763; T', 1765-2212, T', 2214-2224 4-JENN
A;Residues: 1-657, FR, 899-864, FR, 866-1864, FR, 866-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 PTSPTATSTTPSRYKTEL----CRTFSESGRCRYGAKCOFAHGLGELRQANRHPKYKTE 145
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                  MKGASRSPE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 LAHQIYQ------FTDKDKDNVAP-----RSKISPQGYGRRRRSLPEAGPGR
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A; Residues: 1188-1215,1315-2224 <KA2>
A; Residues: 1188-1215,1315-2224 <KA2>
A; Cross-references: GB:M14335
A; Note: parts of this sequence were determined by protein sequencing
R; Keller, F.G.; Ortel, T.L.; Quinn-Allen, M.A.; Kane, W.H.
B; Cheller, F.G.; Ortel, T.L.; Quinn-Allen, M.A.; Kane, W.H.
A; Title: Thrombin: catalyzed activation of recombinant human factor 'A; Reference number: A6139; MUID:95210278
A; Contents: annotation; thrombin cleavage sites
                                                                                                                                                                           61;
                                                                              Length 326;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: coagulation labile factor; proaccelerin
                                                                                                                                                                           17;
                                                                              DB 2;
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                                                                                                                                                                           18; Mismatches
                                                                                                                                                                                                                                                                              34 WALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQD-
                                                                   Score 89.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 TLVSSKPQAHGAPAPPSGSAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 PSLSSSSFSPSSSPPPGDLP 226
                                                                        ch 9.5%;
1 Similarity 22.4%;
45; Conservative 1
                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                      Matches
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Gaps

32;

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R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, May 1999
A; Reference number: 221575
A; Accession: T36566
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Mescule type: DAP
A; Mesidues: 1-82 < Coli>A; Residues: 1-82 < Coli>A; Residues: 1-82 < Coli>A; Residues: Greences: EMBL:AL049826; PIDN:CAB42692.1; GSPDB:GN00070; SCOEDB:SCH24.01c
A; Cross-references: EMBL:AL049826; PIDN:CAB42692.1; GSPDB:GN00070; C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
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C; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
A; Genetics:
A; Genetics:
C; Genetics:
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A; Cross-references: EMBL:U80447; PIDN:AAB37808.1; GSPDB:GN00019; CESP:F55F8.4
A; Experimental source: strain Bristol N2; clone F55F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gispecies: Caenchabdilis elegans
Cispecies: Caenchabdilis elegans
Cispecies: Caenchabdilis elegans
Cispecies: Caenchabdilis elegans
Cispacession: T2958
Gistung, S.; Scheet, P.; Kemp, K.
Submitted to the EMBL Data Library, November 1996
A; Description: The sequence of C. elegans cosmid F55F8.
A; Reference number: 220647
A; Reference number: 220647
A; Reference number: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: D
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-----EYRDRDE- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRSPEDSSPDAARIRVK-RYRQS--MNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKD 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 LGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 NVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 PLRRRQSSPMVASPRRRRSPSPERQRKRRSPSDSPPTRRLSTSPIRRRRSPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.2%; Score 87; DB 2; Length 656;
25.4%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 PAGPAPQAPQSPPSRPQHRYEEPELPAPGQGGRE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F55F8.4 - Caenorhabditis elegans
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21.4%; Pred. No. 7.1;
tive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.48; Pic.
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A;Introns: 56/2; 153/1; 320/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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A;Gene: CESP:F55F8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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I66868
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C.Species: Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Sccession: A41870; T35566
R.Calcutt, M.J.; Schmidt, F.J.
D. Bacteriol. 174, 3220-3226, 1992
A.Title: Conserved gene arrangement in the origin region of the Streptomyces coelicolor A; Reference number: Annoise arrangement in the origin region of the Streptomyces coelicolor A; Reference number: MulD:92250416
A; Accession: A41870
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-656 <CAL>
A; Cross-references: GB:M82836; NID:96539740; PIDN:AAA26734.1; PID:g153240
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9
                                                                                                                                                                                                           198 FLDLDLSRIP-CDFYAGSGHKWLLA------PTGVGFLHLAPGRLEELEPTQVS 244
                                                                                                                                                                                                                                                                             72 GASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT-----CTVQKLAHQIYQF 124
                                                                                                                                                                                                                                                                                                                                                                                                      125 TDKDKDNVAPRSKISPQGYGRRRRRSLPEAG-----PGRTLVS-SKPQAHGAPA---- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKDNVAPRSK----ISPQGYGRRRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKKGAGGGQQPAEPSCKINDQKWYVIS-----SSIGSFFAPCLIMILVYVRIYQIA-K 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 FLGADTARLDVASEFRKKWNKWALSRCKRELRMSSSYPTGLADVKAGPAQ-TLIRPQDMK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Gaps
                                                                                                                                                                                                                                                                                                                       57;
                                       Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 450;
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                           63;
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                                    5
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2.7;
         DB
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9.2%; Score 87;
Best Local Similarity 28.9%; Pred. No. 3matches 35; Conservative 14; Mismatci
                                                                                           46; Conservative
                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 PPGTDA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 PPSGSA 178
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                                                                                        Matches
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protein F56B3.4 [imported] - Caenorhabditis elegans
protein F56B3.4 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C; Accession: F88632
R; anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
R; anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C: elegans: a platform for investigating blo A; Title: Genome sequence of the nematode C: elegans; a platform for investigating blo A; Title: Genome sequence of WuID: 99069613; PMID: 9851916
A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A; Note: publishabd errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A; McCession: F88632
A; Accession: Preliminary
A; Molecule type: DMA
A; Molecule type: Maximum type: Maximum type: Molecule type: 
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an alpha2-adrenergic recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: mRNA
A, Residues: 1-450 <CHA>
A, Residues: 1-450 <CHA>
B, Experimental Source: brain
C, Comment: Alpha -2-adrenergic receptor is a predominant catecholamine receptor.
C, Superfamily: vertebrate rhodopsin
C, Superfamily: vertebrate receptor; transmembrane protein
F; 34-59/Domain: hydrophobic <HII>
F; 71-96/Domain: hydrophobic <HII>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dipha-2-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Bate: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
C;Accession: JH0190
R;Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.
Mol. Cell. Blochen. 97, 161-172, 1990
A;Fithe: Molecular cloning, sequencing and expression of an alpha2-adrenerg;
A;Reference number: JH0190; MUID:91125329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 ROSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDKDKDNVAPRSK----ISPQGYGRR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 VIS-----SSIGSFFAPCLIMILVYVRIYQIA-KRRTRVPPSRRGPDACSAPPGGADR
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                                                                                                                                                                         FFRATAGKEPVRSEYRLRRADGSW-AWVIDVGQPRFSADGTFLGYVGSVLDITERRAAE-
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                                                                                                                                                                                                                                                                                                                      125 TDKDKDNVAPRSKISPQGYGRRRRSLPEAGPGRTL--VSSKP--QAHGAP 171
                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 RRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 RPNGLGPERGAGTAGGEAEPLPTQLNGAPGEPAPTRP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%; Score 82.5; Di
25.5%; Pred. No. 6.9;
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A, Map position: 4
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A:Molecule type: DNA
A:Molecu
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**Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A; Reference number: A95262; MUID:21396509; PMID:11481432
                                                                         C; Species: Rattus sp. (rat)
C; Species: Rattus sp. (rat)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 22-Jun-1999
C; Jacession: 166868
R; Jinno, S.; Suto, K.; Nagata, A.; Igarashi, M.; Kanaoka, Y.; Nojima, H.; Okayama, H. EMBO J. 13, 1549-1556, 1994
A; Title: Cdc25A is a novel phosphatase functioning early in the cell cycle.
A; Reference number: 153194; MUID: 94208523
A; Reference number: 168688
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-574 < RESS
A; Residues: 1-574 < RESS
A; Cross-references: GB: D16237; NID: 9484292; PIDN: BAA03762.1; PID: 91008042
C; Superfamily: human protein-tyrosine-phosphatase cdc25A; cdc25-type protein-tyrosine-ph
F; 366-556/Domain: cdc25-type protein-tyrosine-phosphatase homology < PTP>
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26.9%; Pred. No. 16;
tive 18; Mismatches 93
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec.1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C;Accession: B40392
                                                                                                                                                                                                                                              542 YLKSLDFEKIQEMKLEITERFDPKLLEFLKNRGNKASEETQKKPKKISKFKASRQQK--E 599
                                                                                                                                                                                                                                                                                                                                             PQ-DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIXQFT 125
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                           Length 926;
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Query Match

8.6%; Score 81.5; DB 2; Length 9
Best Local Similarity 24.0%; Pred. No. 19;
Matches 29; Conservative 19; Mismatches 64; Indels
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8.6%; Score 81; DB 2
Best Local Similarity 27.3%; Pred. No. 9.5;
Matches 33; Conservative 13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 VSVALMYLGSLAFLGADTAR.....SKPQAHGAPAPPSGSAPHFL 182
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*

					SUMMARIES	
Result No.	Score	% Query Match	% Query Match Length DB	DB	ID	Description
1	947	100.0		22	AAB49697	Human adrenomeduli
7	947	100.0		22	AAB60344	Human adrenomedull
m	817	86.3		22	AAB49698	Porcine adrenomedu
4	817	86.3		22	AAB60345	Porcine adrenomedu
Ŋ	624.5	62.9		22	AAB49699	Rat adrenomedulin
φ	624.5	62.9	185	22	AAB60346	Rat adrenomedullin
7	469	49.5		21	AAG00251	Human secreted pro
œ	305.5	32.3	. ,	22	AAB75122	UspA(1-57)-(A)-(GS
σ	298	31.5		22	AAB75124	UspA(1-84)-(A)-(GS
10	297.5	31.4		22	AAB75123	UspA(1-56)-(DD)-(G
11	289	30.5		22	AAB75111	Glycine extended h

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	77	000		יש ר	170	4 0	AAB75114		Thioredoxin-(68686
	15	283	29.	, o	22	22	AAB75110		Human adrenomedull
	16	283	29.	0	52	22	AAB91759		Adrenomedullin pep
	17	283	29.	თი	2 Z	22	AAE09818		Human adrenomedull
	16	231	24.	v 4	20	7 7 7	AAE09819		Rat adrenomedullin
	20	227	24.	0 (52	22	AAB91765		Adrenomedullin pep
	21	219.5	23.	2 -	53	22	AAB91767 AAR91768		Adrenomedullin pep
	23	181.5	19.	. ~	37	5,5	AAB91761		Adrenomedullin pep
	24	176	18.	٠	33	22	AAB91764		Adrenomedullin pep
	25	163	17.	O1 C	31	18	AAW25160		Human preproadreno
	27	163	17.	N (N	31	222	AAE09827		Human adrenomedull
	28	107	11.	e	20	18	AAW25161		Human proadrenomed
	29	104	11.	0 (50	22	AAB91766		Adrenomedullin pep
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	43	81.5	. ω	9	624	20	AAY26913		Envelope glycoprot
	44	81.5	ω.	91	625	22	AAB19881		Murine leukemia vi
	45	81.5	ω.	9	637	22	AAB19878		Murine leukemia vi
							ALIGNMENT	ENTS	
RESULT AAB4969 ID AA	1LT 1 9697 AAB4	T 1 697 AAB49697 sta	standard;	rd;	Protein		185 AA.		
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A AC	AAB	AAB49697;							
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XX DE	Human	an adrenomedulin	omed	ulin	amino	o acid	id sequence	ge.	
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X X X	4 -	renomedulir	2 ::	급	ary d		der; incor	ence; human.	
SO	Ношо	sapiens							
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AX O		-DEC-2000							
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PI	Yane	anagita T;							
OR DR	WPI;	1; 2001-08 PSDB; AAF2	8075 2913	4 / 09	÷				
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Z Z X	Comi	Composition comprises ad	+ 년	pro	or promoting enomedulin	pa -	ssive	elongation of Vesicle	e smootn muscre
PS	Claim	1;	Page 2	26-27	, 42pp;		Japanese.		

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          This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for releving uninary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the human adrenomedulin protein, which is used in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                      AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                       IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                          Length 185;
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                                                                                                                                                                    Score 947; DB 22;
Pred. No. 2.1e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB60344 standard; Protein; 185 AA.
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21-MAR-2000; 2000JP-0079171.
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                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 37-38;
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                                                                                                                                           185 AA;
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                                                                                                                                           Sequence
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the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence represents human adrenomedullin precursor.
                                                                                                                                                                                                                                           AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
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                                                                                                                         Length 185;
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                                                                                                                     100.0%; Score 947; DB 22; 100.0%; Pred. No. 2.1e-93;
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Sequence Query Match

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Matches

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This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary disorders such as impending urinary incontinence and urinary incontinence and urinary incontinence with overflow. The present sequence represents the porcine adrenomedulin rat, which is used in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for promoting passive elongation of vesicle smooth muscle
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                                    AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ
                                                        4 VSIALMLIGSLAVIGADTARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVP
VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP
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                                                                                                                 IYQFTDKDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                         Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
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                                                                                                                                                                                                                                                                                                                                                                      Rat adrenomedulin amino acid sequence.
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                                                                                                                                                                                                                                                     AAB49699 standard; Protein; 185
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porcine; pig; adrenomedullin; precursor; bradykinin antagonist; uterine contraction inhibitor; premature birth; miscarriage; abortion; dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                            64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123
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                                                                                                               9
                                                                                                                                   4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                               1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                                                                                                                                                     121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                         ö
                                                                          ;
0
                                    Length 188;
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                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 817; DB 22;
Pred. No. 1.9e-79;
0; Mismatches 9;
                                                                      6
                                  Score 817; DB 22;
Pred. No. 1.9e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     porcine adrenomedullin precursor
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 43-44; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                             Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porcine adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                           AAB60345 standard; Protein; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                        10;
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89.1%;
                                  86.3%;
89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-2000; 2000WO-JP04167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 156; Conservative
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-080755/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                    Similarity
À.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF27229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200078339-A1
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Sus scrofa.

AAB60345;

AAB6034 RESULT

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Gaps

Length 185;

63

represents

Sequence Query Match

Local

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AAB60346

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Human; 5' \rm EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 469; DB 21;
Pred. No. 1.6e-42;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                      Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID 4332; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYR 93
                    Human secreted protein, SEQ ID NO: 4332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB75122 standard; Protein; 120
                                                                                                                                                                                                                                   21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                          99US-0122487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93; Conservative
                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-500381/45.
N-PSDB; AAC00257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 AA;
                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                  Homo sapiens
                                                                                                                                                       EP1033401-A2
                                                                                                                                                                                                                                                                        26-FEB-1999;
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                                                                                                                                                                                              06-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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AAB75122
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7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                         Rat; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYQFTDKDKDNVAPRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         э;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 624.5; DB Pred. No. 8e-59; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 48-49; 54pp; Japanese.
                                                   AAB60346 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG00251 standard; Protein; 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.9%;
                                                                                                                                                                    Rat adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-2000; 2000WO-JP04167.
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHIO ) SHIONOGI & CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                         Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF27230.
                                                                                                                                                                                                                                                                                                                             WO200078339-A1.
                                                                                                                             06-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 126;
                                                                                          AAB60346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Gaps

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Synthetic.

06-OCT-2000 (first entry)

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AAG00251 RESULT

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producing the fused
                                                                                       Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                                                                                                           The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fuse protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDS-----SPDAARIRV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                  31.5%; Score 298; DB 22;
57.4%; Pred. No. 6.1e-24;
tive 6; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
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 Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 69-70; 75pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ā
                                                                                                                                                              Claim 17; Page 71; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB75123 standard; Protein; 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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 Mitsuda Y,
                                   WPI; 2001-282044/29.
N-PSDB; AAH19866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-282044/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                     L Similarity
66; Conserv
                                                                                                                                                                                                                                                                                                                                                                              147 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1999;
 rakimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                 adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                    Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 DVNYSDLY-TGLIDVNLG------DMAGS------GSGDAF-----EYRQSMNNFQG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
                                                                                                                                                                                                Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; L.
/.4e-25;
12;
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Pred. No. 7.4e-
3; Mismatches
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                                                                                                                                                                                               Nakayama T,
                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 68; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.3%;
65.0%;
                                                                                     10-OCT-2000; 2000WO-JP07023.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67; Conservative
                                                                                                                                                                                             Takimoto A, Mitsuda Y,
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             WO200127310-A1.
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                                                                                                                       15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
      adrenomedullin precursor. The method comprises: (a) producing the fuse protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                42 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                  Adrenomedullin; glycine extended adrenomedullin; AM: AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                        21; Gaps
                                                                                                                                                                                                              39 DVNYSDLY-TGLIDVNLG------BDDGS------EYRQSMNNFQG 77
                                                                                                                                                DB 22; Length 120;
invention describes a method (M1) for producing
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                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Glycine extended human adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                              102 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
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                                                                                                                                              Score 297.5; DB 22;
Pred. No. 5.3e-24;
3; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                   AAB75111 standard; Protein; 53
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                                                                                                                                               Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                       120 AA;
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                                                                    Gaps
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                                                                                                                  92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDKDNVAPRSKISPQGYG 144
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Pred. No. 1.5e-23;
0; Mismatches 0;
                 Score 289; DB 22;
Pred. No. 1.5e-23;
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30.5%; Scor.
100.0%; Pred. No. 100.0%; O; Mismatches
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53; Conservative 0;
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                                                                  Conservative
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                                        Similarity
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Mitsushima

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The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications, AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
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                                                                                           Nakayama T,
                                                                                                                                                                                                                                                                Claim 17; Page 49-50; 75pp; Japanese
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                                                                                                                                                                                    Producing adrenomedullin useful application comprises producing recombinant host
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                 99JP-0294147
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Best Local Similarity
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N-PSDB; AAH19810
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                                                                         Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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                                   Linker peptide-adrenomedullin (AM) precursor protein.
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100.0%; Pred. No. 1.8e-23;
tive 0; Mismatches 0;
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RESULT 14 AAB751

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Gaps

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The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                              Query Match

29.9%; Score 283; DB 22; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.4e-23;
Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                              52 AA;
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       888888888888
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Search completed: October 17, 2002, 15:21:13 Job time : 31.4202 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 17, 2002, 15:20:12 ; Search time 6.51466 Seconds (without alignments)

(without alignments)
742.931 Million cell updates/sec

Perfect score: 655 Sequence: 1 ARLDVASEFRKKWNKWALSR......FTDKDKDNVAPRSKISPQGY 125

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	6 homo	s sns 9	O62827 bos taurus	O77559 canis famil	P43145 rattus norv	P97297 mus musculu	P41593 mus musculu	Н				P14480 rattus norv	-		P07761 brassica ol	P32255 dictyosteli	P49178 zea mays (m	٣	S	_	4		Q04604 rana nigrom		P30082 rattus norv	Q99504 homo sapien		chlam	4	5 bacil	omod 3	Q9p2g4 homo sapien	stre
SUMMARIES	er er	: 8	ADML_PIG	ADML_BOVIN	ADML_CANFA	ADML_RAT	ADML_MOUSE	PTRR_MOUSE	PTRR_RAT	FIBB_PETMA	FA5_HUMAN	PRI1_SCHPO	FIBB_RAT	VP13_YEAST	MOXJ_METEX	SLS6_BRAOL	TBA_DICDI	GBB_MAIZE	SKI8_YEAST	GUN5_BACAG	TBAA_SCHCO	TBA2_EMENI	SC14_YARLI	TYRO_RANNI	TOP5_BPT4	GLR_RAT	EYA3_HUMAN	RPOB_CHLMU	RPOB_CHLTR	CENF_HUMAN	GUN2_BACS4	FIBB_HUMAN	- 1	CEFD_STRCL
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Q01337 mus musculu P22086 rattus norv	P47871 homo sapien P43811 haemophilus	Q24546 drosophila P29713 anabaena sp	Q08369 mus musculu P05432 rattus norv	Q02020 gallus gall	P18419 mus musculu	P24820 arabis mosa
A2AC_MOUSE A2AC_RAT	GLR_HUMAN SPOT_HAEIN	SYN_DROME Y457_ANASP	GAT4_MOUSE G33 RAT	FIBB_CHICK	SVS4_MOUSE	VP3_ARMV
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458 458	677	980 215	440 459	463	108	360
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63.5	63.5	63.5 63	63 63	63	62.5	62.5
34 35	36	9 6 9 6	40	42	44	45

ALIGNMENTS

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Champion H.C., Nussdorfer G.G., Radowitz P.J.;
Structeractivity relationships of adrenomedullin in the circulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and adrenal gland.";
Regul. Pept. 85:1-8(1999).
-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
--AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE
PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE
KIDNEY, AM IS DIUNETIC AND NATRIURETIC, AND BOTH AM AND PAMP
                                                                                                                                                                                                                                                 TISSUE-Pheochromocytoma;
MEDLINE-93143928; PubMed-7688224;
Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
"Cloning and characterization of cDNA encoding a precursor for human
                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-2(terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                          Homo sapiens (Human).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
Matsuo H., Eto T.;
"Adrenomedullin: a novel hypotensive peptide isolated from human
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
MEDLINE=94354869; PubMed=8074714;
IShimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H., Kitamura K., Eto T., Matsuo H.;
"Genomic structure of human adrenomedullin gene.";
Biochem. Biophys. Res. Commun. 203:631-639(1994).
                                                                                                                                                                                                                                                                                                                     adrenomedullin.";
Biochem. Biophys. Res. Commun. 194:720-725(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 192:553-560(1993).
185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Samson W.K.;
"Proadrenomedullin-derived peptides.";
Front. Neuroendocrinol. 19:100-127(1998).
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVIEW.
MEDLINE=20053666; PubMed=10588445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Pheochromocytoma;
MEDLINE=93249425; PubMed=8387282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98240137; PubMed-9578982;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 95-146.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pheochromocytoma."
ADML_HUMAN P35318;
                                                                                                                           ADM OR AM.
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SEQUENCE FROM N.A
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                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN PITUITARY GLAND, BOTH PRETIDES AT PHYSIOLOGICALLY RELEVANT DOSES INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME, ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0cT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                      PROADRENCMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION (G-42 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
64C7D2A0B4654DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                 Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                  -!- SUBCELLULAR LOCALLON.
-!- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN FILL ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 655; DB 1;
Pred. No. 1e-61;
; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                             ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 AA
                                                                                                                                                                                                                                                                                                           InterPro; IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                              EMBL; D14874; BAA03589.1; -.
EMBL; S73906; AAC60642.1; -.
EMBL; D43639; BAA07756.1; ALT_SEQ.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                           146
185
115
                                                                                                                                                                                                                                                              PIR, JN0476; JN0476.
PIR, JN0684; JN0684.
PIR; JC2351; JC2351.
MIM; 103275; -.
                                                                                                                                                                                                                                                                                                                                                Hormone; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 AA;
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                                                        VESSELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 125;
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SEQUENCE
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P53366;
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PROPEP
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last anoncation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                            Eto T.;
nd cloning
                                                                                                                                                                                                                                Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y., Kawamoto M., Minamino N., Matsuo H., Eto T.; Identification and hypotensive activity of proadrenomedullin N-terminal 20 peptide (PAMP)."; FEBS Lett. 351.35-37(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 ARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hormone; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL \scriptstyle 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREPROAM C-TERMINAL FRAGMENT (BY SIMILARITY).

    Ichiki Y., Matsuo H., Et
porcine adrenomedullin and

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 611; DB 1; Length 18
Pred. No. 4.4e-57;
8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71749460F5660A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 AA.
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Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDUIN.
                                            Kitamura K., Kangawa K., Kojima M.,
"Complete amino acid sequence of por
                                                                                                                                                                                      TISSUE-Adrenal medulla;
MEDLINE-94357274; PubMed-8076689;
                 MEDLINE-94139945; PubMed-8043068;
                                                                                            of cDNA encoding its precursor.";
FEBS Lett. 338:306-310(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20893 MW;
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Matches 114; Conservative
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TISSUE-Adrenal medulla;
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146
188
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146
188 AA;
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062827;
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ADML_BOVIN
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Imoto I., Jougasaki M.;
'Cloning of cDNA encoding canine adrenomedullin.";
                                                                                  SEQUENCE FROM N.A.
                       SEQUENCE FROM N.A
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45
95
148
NCBI_TaxID=9615;
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P43145;
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                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADML_CANFA STANDARD; PRT; 188 AA.
077559, O9TVC9;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM Precursor [Contrains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                               PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
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                                                                                                                   Barker S., Wood E., Clark A.J.L., Corder R.; "Cloning of bothe preproadrenomedullin and inhibition of its basal expression in vascular endothelial cells by staurosporine."; Life Sci. 62:1407-1415(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
AMIDATION (G-147 PROVIDE AMIDE GROUP)
                                   Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                -i- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN CIRCULATION CONTROL (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                          Cleavage on pair of basic residues; Signal. 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.5%; Score 606; DB 1; Length 188; Larity 92.0%; Pred. No. 1.5e-56; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      PREPROAM C-TERMINAL FRAGMENT
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                                                                                                                                                                                                                                                                                                                                                                                                        ADRENOMEDULLIN.
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InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                       MEDLINE=98244567; PubMed=9585168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AA;
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es 115; Conserv
                                                                              SEQUENCE FROM N.A.
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148
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                                                       NCBI_TaxID=9913
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                                                                                            TISSUE=Aorta;
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PROPEP
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                                                                                 MEDILINE=99002704; PubMed=9788655;
MEDILINE=99002704; Nodada K., Kangawa K.;
Ono Y., Kojima M., Okada K., Kangawa K.;
"cDNa Clohing of canine adrenomedullin and its gene expression in the heart and blood vessels in endotoxin shock.";
Shock 10:243-247(1998).
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 ARLDVASEFRKKWNKWAVSRGKRELRVSSSYPTGLAEVKAGPAQTLIRTQDVKGASRNPQ 81
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                                                                                                                                                                                                                                                 -! - FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
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AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
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llarity 90.4%; Pred. No. 1.3e-55;
Conservative 6; Mismatches 6; Indels
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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809D6A64F98F5578 CRC64;
                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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ADRENOMEDULLIN.
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188
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41
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Matches 113; Conserv
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musculus (Mouse).

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ADML_MOUSE STANDARD; PRT; 184 AA.
P97297; P97453;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
               ADML_MOUSE
                                                                                                                              Mus
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                                                                                                                                                                                                                 Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N., Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Fewerstein G.Z.; "Discovery of adrenomedullin in rat ischemic damen evidence for its role in exacerbating focal brain ischemic damen."; Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-Adrenal gland;
MEDLINE-93384621; PubMed-7690563;
Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
Matsuo H., Eto T.;
"Molecular cloning and biological activities of rat adrenomedullin, a
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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21 BY SIMILARITY.
41 PROADERSHOMEDULLIN N-20 TERMINAL PEPTIDE.
91 BY SIMILARITY.
143 ARRENOMEDULIN.
185 PREPROAM C-TERMINAL FRAGMENT (BY
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-!- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY, HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
-!- SIMILARITY: BELONGS TO THE ADRENONEDULLIN FAMILY.
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AMIDATION (G-42 PROVIDE AMIDE GROUP)
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35CAD9A9DD19AE35 CRC64;
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                                                                                                                                        hypotensive peptide.";
Blochem. Blophys. Res. Commun. 195:921-927(1993)
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BY SIMILARI
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Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
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                                        NCBI_TaxID-10116
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PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                      Yotsumoto S., Ko M.S.H.;
"Expression of mouse adrenomedullin gene in trophoblastic glant
cells at the implantation site.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                      Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; Genomic organization, expression, and chromosomal mapping of the mouse adrenomedullin gene"; Genomics 37:395-399(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION (G-145 PROVIDE AMIDE GROUP)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
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PREPROAM C-TERMINAL FRAGMENT
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C88C99045A79C898 CRC64;
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Pred. No. 2e-3
8; Mismatches
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InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted
                                                                                                                                      MEDLINE-97092892; PubMed-8938454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D78349; BAA11367.1; -. EMBL; U77630; AAB36535.1; -.
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68.9%;
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                                           NCBI_TaxID=10090;
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45
95
151
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                                                                                                                   STRAIN-129/SV
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                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
MCCUalg K.A., Clarke J.C., White J.H.;

MACLecular cloning of the gene encoding the mouse parathyroid hormone/parathyroid hormone-related peptide receptor.";

Proc. Natl. Acad. Sci. U.S.A. 91:501-5055(1994).

-!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                           PTRR_MOUSE STANDARD; PRT; 591 AA.
P41593; 062119;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Parathyroid hormone/parathyroid hormone-related peptide receptor
                                                                                                                                                                                                                                                                                                                                                   STRAIN=C3H/HEHA;
MEDLINE=95034305; PubMed=7524627;
Karperlan M., van Dijk T.B., Hoeijmakers T., Cremers F.,
Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
Expression pattern of parathyroid hormone/parathyroid hormone
related peptide receptor mRNA in mouse postimplantation embryos
indicates involvement in multiple developmental processes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCRDb; GCR_1614; -.
MGD; MGI:97801; Pthr.
InterPro; IPR000832; GPCR_secretin.
InterPro; IPR001879; hormn_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L34611; AAA40011.1; -. EMBL; L34608; AAA40011.1; JOINED. EMBL; L34607; AAA40011.1; JOINED. EMBL; L34609; AAA40011.1; JOINED. EMBL; L34610; AAA40011.1; JOINED. HSSP; Q03431; 1BL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94255468; PubMed-8197183;
                                                                                                                                                                                                                                  precursor (PTH/PTHR receptor)
PTHR1 OR PTHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00249; GPCRSECRETIN.
SMART; SM00008; HormR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X78936; CAA55536.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mech. Dev. 47:29-42(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00002; 7tm_2; 1.
Pfam; PF02793; HRM; 1.
                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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GY 144
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                                          GY 125
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                                          124
                                                                                                                  RESULT 7
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TISSUE-Bone;
MEDLINE-92212903; PubMed-1313566;
Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,
Kronenberg H.M., Segre G.V.;
Kronenberg H.M., of a common receptor for parathyroid hormone and
parathyroid hormone-related peptide from rat osteoblast-like cells: a
single receptor stimulates intracellular accumulation of both cAMP
and inositol trisphosphates and increases intracellular free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARATHYROID HORMONE/PARATHYROID HORMONE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                                                                        4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

MISSING (IN REF. 2).

MISSING (IN REF. 2).
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-CTT-2001 (Rel. 40, Last annotation update)
Parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PHYPTHR receptor).
PIHRI OR PIHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%; Score 77; DB 1; Length 591; 32.5%; Pred. No. 1.6;
                                                                                                                                              1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GA -> VS (IN REF. 2).
F7876F8D388BDDFD CRC64;
                                                                                                                 RELATED PEPTIDE RECEPTOR
                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
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1D388PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66313 MW;
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Matches 26; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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2220
2240
2240
2283
3307
3321
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4441
1061
1161
1166
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444
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TRANSMEM
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CARBOHYD
CARBOHYD
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TRANSMEM
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DOMAIN
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TRANSMEM
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CARBOHYD
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5;

MEDLINE-94292182; Pubmed-8020952;

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525 ATTNGHSOLPGHAKPGA 541
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                                                                    FIBB_PETMA
                                                      RESULT 9
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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           Pausova Z., Bourdon J., Clayton D., Mattel M.-G., Seldin M.F., Janicka N., Stylere M., Szpirer G.; Stylere C.; Triviare M., Szpirer G.; Szpirer G.; Tconing of a parathyroid hormone/parathyroid hormone-related peptide receptor (PTHR) cDNA from a rat osteosarcoma (UMR 106) cell line: chromosomal assignment of the gene in the human, mouse, and rat Genomics 20:20-26(1994).
                                                                                                      FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR ARATHYROID HORMONE-RELATED REPTIES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WICH ACTIVATE ABDIVALE CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARATHYROID HORMONE/PARATHYROID HORMONE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPP 524
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                                                                                                                                                                                -1 - SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 75; DB 1; Length 591;
Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                          protein
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                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane
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6 (POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                     GCRDb; GCR_0038; ...
InterPro: IPR000083; ...
InterPro: IPR000082; GPCR_secretin.
InterPro: IPR00002; 7tm_2; 1.
Pfam; PF020002; 7tm_2; 1.
PRINTS; PR00249; GPCRSECRETIN.
SMART; SM000008; HOFMR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
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                                                                                                                                                                                                                                                                                                                   EMBL; M77184; AAA41811.1; -. EMBL; L19475; AAA68098.1; -. HSSP; Q03431; 1BL1.
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32.5%;
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                                                                                                                                                                                                                                                                                                                                                           GCRDb; GCR_0206; -.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 37-477 FROM N.A.
MEDLINE-87076582; pubmed=3790537;
MEDLINE-87076582; pubmed=3790537;
Bohonus V.L., Doolittle R.F., Pontes M., Strong D.D.;
"Complementary DNA sequence of lamprey fibrinogen beta chain.";
Blochemistry 25:6512-6516(1986).
- 1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COPACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO BACH OTHER BY DISULLEDE BONDS.
-1- MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XILIA WHICH CATALYZES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                          Cottrell B.A., Doolittle R.F.; "Amino acid sequences of lamprey fibrinopeptides A and B and characterizations of the junctions split by lamprey and mammalian
                                                                                                            Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                      01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH THE ALPHA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH THE ALPHA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH THE GAMMA CHAIN)
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A03124; A03124.
HIS; A25022; A25052.
HISSP: P020755; IFZF.
InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; fibrinogen_C: 1.
SMART; SM00186; FB6; 1.
Blood coagulation; Plasma; Sulfation; Glycoprotein.
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N-LINKED (GLCNAC.
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 477 AA.
                                                                                                                                                                                                                                                                                                                 Biochim. Blophys. Acta 453:426-438(1976).
   PRT;
                                                                                                                                                                                                                          MEDLINE=77065679; PubMed=999898;
                                      21-JUL-1986 (Rel. 01, Created)
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 STANDARD;
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37
477
13
27
84
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                                                                                                                                                                                                         SEQUENCE OF 1-36.
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                                                                                                                                                                      NCBI_TaxID=7757
FIBB_PETMA
P02678;
                                                                                                                                                                                                                                                                                                    thrombins.
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CARBOHYD
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                                                                                                                                                                                                                                                              51 DMKG-----ASRSPEDSSPDAARIRVKRYRQSMNN--FQGLRSFGCRFGTCTVQKLAH 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-1600 FROM N.A. MEDINE-88107560; Pubmed=2827731; Kane W.H., Ichinose A., Hagen F.S., Davie E.W.; "Cloning of cDNAs coding for the heavy chain region and connecting region of human factor V, a blood coagulation factor with four types
                                                                                                                                                                     Gaps
                                                                                                                                                                                                  2 RLDVASEFRKKWNKW-----ALSRGKRELRMSSSYPTGLADV----KAGPAQTLIRPQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., Aldape R.A., Hewick R.W., Kaufman R.J., Mann K.G.; "Complete cDNA and derived amino acid sequence of human factor V."; Proc. Natl. Acad. Sci. U.S.A. 84:4846-4850(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86313665; PubMed=3092220;
Kane W.H., Davie E.W.;
"Cloning of a cDNA coding for human factor V, a blood coagulation
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxID=9606;
                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989 (Rel. 12, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Coagulation factor V precursor (Activated protein C cofactor).
                             THE GAMMA CHAIN)
INTERCHAIN (WITH THE ALPHA CHAIN)
                                                                                                                                    Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Fibroblast;
MEDLINE-93203619; PubMed-8454869;
Shen N.L., Fan S.-T., Pyati J., Graff R., Lapolla R.J.,
Edgington T.S.;
                                                                                                                                                                   59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92232668; PubMed-1567832;
Cripe L.D., Moore K.D., Kane W.H.;
"Structure of the gene for human coagulation factor V.";
Biochemistry 31:3777-3785(1992).
                                                                                                       B8A95E7E32D09D18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor homologous to factor VIII and ceruloplasmin.";
Proc. Natl. Acad. Sci. U.S.A. 83:6800-6804(1986).
                                                                                                                                   DB 1;
            (BY SIMILARITY).
INTERCHAIN (WITH T
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                                                                                                                                                                                                                                                                                                                                                                                                                                      2224 AA.
                                                                                                                                                   ; Pred. No. 4.9;
15; Mismatches
                                                                                                                                      Score 71.5;
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MEDLINE-87260886; Pubmed-3110773;
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                                                                                                       54270 MW;
                                                                                                                                      10.9%;
26.3%;
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                                                                                                                                                                     36; Conservative
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259
425
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P12259; 014285;
01-0CT-1989 (Rel
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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-1- DISEASE: OWREN PARAHEMOPHILIA, AN HEMORRHAGIC DIASTESIS, IS DUE
TO A DEFICIENCY OF FACTOR V. OTHER DEFECTS IN FS RESULTS IN A
FORM OF THROMBOPHILIA KNOWN AS APC RESISTANCE (APCR). THE APCR
MUTATION IS FOUND IN ABOUT 5% OF THE POPULATION WHICH SUGGEST THAT
A SLIGHT THROMBOTIC TENDENCY MAY CONFER SOME ADVANTAGE IN FETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activated protein C.";
Nature 389:64-67(1994).

-:- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES

-:- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES

WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.

-:- SUBMUNIT: Factor V as is composed of a heavy chain and a light chain, noncovalently bound. The interaction between the two chains is calcium-dependent.
                                                                                                                                            "Posttranslational sulfation of factor V is required for efficient thrombin cleavage and activation and for full procoagulant activity."; Biochemistry 33:6952-6959(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- DOMAIN: DOMAIN B CONTAINS 35 X 9 AA TANDEM REPEATS, AND 2 X 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF 2 PLASTOCYANIN-LIKE REPEATS.
-!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
-!- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94217810; PubMed-8164741;
Bertina R.M., Koeleman B.P.C., Koster T., Rosendaal F.R.,
Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.;
"Mutation in blood coagulation factor V associated with resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Thrombin activates factor V proteolytically to the active cofactor, factor Va (formation of a heavy chain at the N-terminus and a light chain at the C-terminus).

PTM: SULRATION IS REQUIRED FOR EFFICIENT THROWBIN CLEAVAGE AND
                                                                                                                                                                                                                                                                                                                                                                                 Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A., Kim S.W., Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T., Kane W.H., Fuentes-Prior P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Crystal structures of the membrane-binding C2 domain of human
                                                                                                                                                                                                                                                                        Hortin G.L.; "Sulfation of tyrosine residues in coagulation factor V."; Blood 76:946-952(1990).
                                                                                                                  Pittman D.D., Tomkinson K.N., Michnick D., Selighsohn U.,
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serine protease cofactor factor V is synthesized
                                                                                                                                                                                                                                                                                                                                                  ANGSTROMS) OF 2065-2224.
                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTRO) MEDLINE=20052169; Pubmed=10586886;
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                                                                                                                                                                                                                                                    MEDLINE=90366699; PubMed=2168225;
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                                                                                              MEDLINE=94264012; PubMed-8204629;
                                      Immunol. 150:2992-3001(1993)
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AAB59401.1;
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AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402:434-439(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation factor V.
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L32757;
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L32761;
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                          lymphocytes
                                                                              SULFATION
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EMBL;
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EMBL;

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10.8%; 22.6%;
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             1346
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NCBI_TaxID=4896;
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973 ISPQ 976
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InterPro: IPR001117; Cu-oxidase.
InterPro: IPR000421; FA38_C.
InterPro: IPR000421; FA38_C.
Pfam; PF00034; Cu-oxidase; 3.
Pfam; PF000734; F5_F8_type_C; 2.
SNART; SM00211; FA58C; 2.
PROSITE; PS01286; PA58C_1; 2.
PROSITE; PS01286; FA58C_1; 2.
Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen; Repeat; Polymorphism; Disease mutation; Thrombophilia; 3D-structure.
SIGNAL
29 2224 COAGULATION FACTOR V.
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35 X 9 AA APPROXIMATE TANDEM REPEATS OF
[TNP]-L-S-P-D-L-S-Q-T.
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ACTIVATION PEPTIDE (CONNECTING
LIGHT CHAIN.
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1-1.
1-2.
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PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
F5/8 TYPE A 2.
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PLASTOCYANIN-LIKE 4.
  JOINED.
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                                                                                                AABS9401.1;
AABS9401.1;
AABS9401.1;
AABS9401.1;
AABS9401.1;
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AAB59401.1;
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L32774;
L32775;
L32776;
L32777;
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                                                                                                                                                 L32768;
L32769;
L32770;
L32771;
L32771;
                                            EMEL, 132764, EMEL, 132765, EMEL, 132766, EMEL, 132769, EMEL, 132779, EMEL, 132771, EMEL, 132771, EMEL, 132777, EMEL, 133777, EM
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                                                                                                                                                                                                                                                                             --SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSK 119
                                                                                                                                                                                                                                                                                               933 LLKQSNSSKILVGRWHLAS-------BKGSYEIIQ--DTDEDTAVNNWL 972
                                                                                                                                                                                                                                   Gaps
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InterPro; IPR002755; DNA_primase_S.
Pfam; PF01896; DNA_primase_S; 1.
Transferase; DNA replication: DNA-directed RNA polymerase; Primosome.
ACT_SITE 66 66 POTENITAL.
                                                                                                                                                                                                                4 DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPED-- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-972;
Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (AuG-1997) to the EMBL/Genbank/DDBU databases.
-!- FUNCTION: DNA PRIMARE IS THE POLYMERASE THAT SYNTHESIZES SMALL
RNA PRIMERS FOR THE OKAZAKI FRAGMENTS MADE DURING DISCONTINUOUS
-!- SUBUNIT: HETERODIMER OF A SMALL SUBUNIT AND A LARGE SUBUNIT.
-!- SIMILARITY: BELONGS TO THE EUKARYOFIC PRIMASE SMALL SUBUNIT
FAMILY.
                                                                                                                                                                                    24;
                                                                                                                                                      DB 1; Length 2224;
                                                                                                                                                                                   52; Indels
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POTENTIAL.
71526FFAF7C2BBFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIL_SCHPO STANDARD; PRT; 454 AA. 014215.
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
Probable DNA primase small subunit (EC 2.7.7.-).
                                                                                                                                                    ; Score 71; DB
; Pred. No. 30;
20; Mismatches
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454 AA;
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VP13_YEAST
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                                     6;
                                                                             -----QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 102
                                                                                                                                         331 RLDVEVSRHLNHLLKSPFCVHPGTSRVCVPIDIERMDSFNPLK-----VPTVNDLLQE 383
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
                                                           4 DVASEFRKKW------NKWA----LSRGKRELRMSSSYPTGLADVKAGPAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143.
MEDLINE-89378771; PubMed-2673932;
Eastman E.M., Gilula N.B.;
"Cloning and characterization of a cDNA for the B beta chain of rat
fibrinogen: evolutionary conservation of translated and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=WISTAR; TISSUE-Liver;
MEDLINE-87134033; PubMed=3817019;
Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
"Molecular cloning of mRNA sequences transfently induced during rat
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95143386; PubMed-7841303; Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.; Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.; "Cloning of the complete coding sequence of rat fibrinogen B beta chain cDNN: interspecies conservation of fibrin beta 15-42 primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell Res. 169:47-56(1987).
FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-26 FROM N.A.
MEDLINE-44194000; PubMed-6232608;
FOWIKES D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
Potential Datasis for regulation of the coordinately expressed fibrinogen genes: homology in the 5' flanking regions.";
Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
           DB 1; Length 454;
                                    43; Indels
                      ; Pred. No. 8.4; 20; Mismatches
                                                                                                                                                                                                                                                           479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 19-32.
Blomback B., Blomback M., Grondahl N.J.;
Bludies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure.";
Blood Coagul. Fibrinolysis 5:487-496(1994).
         10.5%; Score 69; 24.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibrinogen: evolutionary cons
3'-untranslated sequences.";
Gene 79:151-158(1989).
                                  32; Conservative
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13,
01-OCT-1996 (Rel. 34,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                  103 IYQFTDKDKDN 113
                                                                                                                                                                                   384 L----DKNSQN 390
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Exp. Cell Res. 169:4
                      Local Similarity
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         Query Match
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MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. SIMILARITY: CONTAINS I FIBRINOGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 RQDGSVDFGRKWDPYKKGFGNIATNEDTKKYCGLPGEYWLGNDKISQLTRIGPTELLIEM 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFG-----TCTVQKLA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | BY SIMILARITY | BY SIMILARIT
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INTERCHAIN (WITH THE ALPHA CHAIN)
(BY SIMILARITY).
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BY GYMYTH THE GAMMA CHAIN)
RY CYNYYLLARITY).
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EMBL; M27220; AAA41160.1; --
EMBL; M27320; AAA41160.1; --
EMBL; M36502; AAA41159.1; --
EMBL; M5629; A65299.
PIR; A65299; A65299.
PIR; PE0010; PE0010.
HSSP; P26675; IFE0018; Fibrinogen_C.
FFAM; PF00147; fibrinogen_C.
Pfam; PF00147; fibrinogen_C.
Pfam; PF00147; Fibrinogen_C.
Pfam; PF00186; FEG; 1.
SMART; SM00186; FEG; 1.
Blood coagulation; Plasma; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRINGEN BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VP13_YEAST STANDARD; PRT; 3144 AA.
OQ07878; 000040;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Vacuolar protein sorting-associated protein VPS13.
VPS13 OR SOII OR YLL040C.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68.5; DB 1;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : |: |: | : | : | 388 HNGMFFSTYDRDNGWVTTDPRKQCSKE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 HQIYQFTDKDKDN-----VAPRSKISPQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5%; 20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
479
32
211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441
445
467
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479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219
229
412
382
382
439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM.
Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
Nasrallah J.B., Sao T.-H., Goldberg M.L., Nasrallah M.E.;
-i- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
(THE INABILITY OF ELOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
-i- TISSUE SPECIFICITY: STIGMA.
-i- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.; "Amino-acid sequence of glycoproteins encoded by three alleles of the S locus of Brassica oleracea."; Nature 326:617-619(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.; "A cDNA clone encoding an S-locus-specific glycoprotein from Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ALSRGKRELRMS----SSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVK 72
extorquens AM1 moxF and
              Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Indels
                                                                                                                                                                                                                                                                                                                                                           1 25 POTENTIAL.
26 300 MOXJ PROTEIN.
300 AA; 32425 MW; BC347551D51B542F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-A0G-1988 (Rel. 08, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
S-locus-specific glycoprotein S6 precursor (SLSG-6).
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
 "Nucleotide sequence of the Methylobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%; Score 67.5; Di
30.1%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
                                                                                                                                                                                                                                                                                                                           SMART; SM00062; PBPb; 1. Signal; Methanol utilization; Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 RYRQ---SMNNFQGLRSFGCRFGTCTVQKLAHQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 AAEQPPLSMKDGSGLEN---RIATTVAEAMGRK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica oleracea (Cauliflower).
                                                                                                                                                                                                                                                                                           PIR; JQ0707; JQ0707.
InterPro; IPR001638; SBP_bac_3.
                                                                                                                                                                                                                                                                           EMBL; M31108; AAA25381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 22-435 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 318:263-267(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B.OLERACEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLS6_BRAOL
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
 В
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                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luo W., Chang A.;
Unpublished observations (XXX-1997).
-!- FUNCTION: PROMOTES ENDOSOMAL CYCLING OF TGN MEMBRANE PROTEINS BY
MODULATING THE FUNCTION OF TWO CYTOSOLIC TGN LOCALIZATION SIGNALS.
-!- SIMILARITY: SOME, TO S.POMBE SPBC16C6.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1354 SGGKGEIKSPSPDPASL----SSESERTATPQSLQGSNKSNIKNPEQKYLDFSFKAPKIA 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 VKRYRQ-----SMNN------FQGLRSFGCRFG---TCTVQKLAHQIYQFTDKD----K 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRS----PE----DSSPDAARIR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-AMI / NCIB 9133;
MEDLINE-90337342; PubMed-2116368;
Anderson D.J., Morris C.J., Nunn D.N., Anthony C., Lidstrom M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Methylobacterium group; Methylobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3144;
                                                                                                                                     SEQUENCE OF 1-1360 FROM N.A.
Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3144 AA; 357843 MW; BEE9B55BA2AD515B CRC64;
                                                                                   Brickner J.H., Fuller R.S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          Wedler H., Wedler E., Scharfe M., Wambutt R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                        Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
 Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 14, Last sequence update) (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68.5; DB
Pred. No. 82;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                        SEQUENCE OF 1095-3144 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF001317; AAC08284.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 273144; CAA97490.1; -. EMBL; 273145; CAA97491.1; -. SGD; SO003963; VPS13. SEQUENCE 3144 AA; 357843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methylobacterium extorquens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MoxJ protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : |:||
1466 DNKHTELIPKSK 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 DN----VAPRSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         CHARACTERIZATION
               NCBI_TaxID-4932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=408;
                                                                   STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOXJ_METEX
P16028;
                                                                                                                                                                        Moestl D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 RPQDMK-----GASRSPEDSSPDAARIRVKRYRQSMNNF---QGL----FGCR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLDVASEFRKKWNKWALSRGKRELRMSSS------YPTG--LADVKAGPAQTLI 47
                                                                                                                                                                                                                                                                                                                                                                                436 S-LOCUS-SPECIFIC GLYCOPROTEIN S6.
46 N-LINKED (GLCNAC. . .) (POTENTIAL).
114 N-LINKED (GLCNAC. . .) (POTENTIAL).
121 N-LINKED (GLCNAC. . .) (POTENTIAL).
245 N-LINKED (GLCNAC. . .) (POTENTIAL).
261 N-LINKED (GLCNAC. . .) (POTENTIAL).
261 N-LINKED (GLCNAC. . .) (POTENTIAL).
390 N-LINKED (GLCNAC. . .) (POTENTIAL).
390 N-LINKED (GLCNAC. . .) (POTENTIAL).
390 N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
-!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN KINASE RECEPTOR (ZMPK1).
                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.2%; Score 67; DB 1; Length 436; 25.3%; Pred. No. 13; tive 22; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 FSGIPEDQKLSYMVINFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 F-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 125
                                                                                                                                                                            EMBL; Y00268; CAA68375.1; -.
EMBL; X03170; CAA56934.1; ALT_INIT.
PIR, A27827; A27827.
InterPro; IPR001480; B_lectin.
InterPro; IPR003609; Pan_app.
InterPro; IPR008589; Slocus_glycop.
Fam; PF001453; Agglutinin; 1.
Pfam; PF001453; Agglutinin; 1.
SMART; SM00108; B_lectin; 1.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Conservative
                                                                                                                                                                                                                                                                                                                                                                  436
446
46
64
114
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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- protein search, using sw model OM protein October 17, 2002, 15:20:13 ; Search time 11.8078 Seconds (without alignments) 1017.222 Million cell updates/sec Run on:

US-10-018-924-2_COPY_22_146 Perfect score:

1 ARLDVASEFRKKWNKWALSR......FTDKDKDNVAPRSKISPQGY 125 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR_71:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	adrenomedullin pre	adrenomedullin - p	Id	parathyroid hormon			conserved hypothet	fibrinogen beta ch	. coaqulation factor		probable DNA prima	fibrinogen beta ch		hypothetical prote	VPS13 protein - ye	Ω	rod shape-determin	probable phospholi	methanol oxidation	S-locus-specific q		GTP-binding protei	antiviral protein	ARHGAP9 protein -		w	tubulin alpha-2 ch	phosphatidylinosit	monophenol monooxy
SUMMARIES	ID	JN0684	S41600	JN0766	S44203	159297	154195	C95367	A25052	KFHU5	T08036	T39017	A05299	F88632	н86389	S64791	T28776	T31120	T09344	JQ0707	A27827	S03701	T02085	S30023	JC7701	S57488	T47857	S13337	S43745	9
	DB			7							7	~	7	7	7	~				~										
	Length	185	188	185	591	583	591	1051	479	2224	380	454	328	926	1196	3144	168	347	828	300					731	1050	297	451	497	532
dР	Query Match	100.0	93.3	70.0	٠		11.5	11.5	•	•		10.5		10.5	10.5	10.5	10.4	10.4	10.4	10.3	10.2	10.2	10.1	10.1	10.1	10.1	10.0	10.0	10.0	10.0
	Score	655	611	458.5	77	92	75	^	71.5	71	69	69	68.5	68.5	68.5	68.5	89	89	89	67.5	o	66.5	99	99	99	99	65.5			65.5
	Result No.	Н	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	tubulin alpha chai	hypothetical prote	glucagon receptor	membrane alanyl am	hypothetical prote	cell-cycle-depende	DNA-directed RNA p	DNA-directed RNA p	coenzyme F420-depe	cellulase (EC 3.2.	qlucose 6 phosphat	hypothetical prote
AD1868	T16112	н81690	T24283	S71574	G75453	J01957	G81856	T06636	PC4035	H71529	G81686	D70669	B25156	T51467	T25413
7	~	~	~	N	a	~	~	N	ď	7	~	~	~	N	7
727	1116	253	305	380	428	485	867	924	1017	1252	1252	381	409	417	444
10.0	10.0	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	9.6	8.6	9.6	9.8
65.5	65.5	65	65	65	65	65	65	65	65	65	65	64.5	64.5	64.5	64.5

ALIGNMENTS

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Gaps ó

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100.0%; Score 655; DB 2; 100.0%; Pred. No. 2.6e-61; ive 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 125; Conservative

Length 185; Indels ~

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parathyroid hormone-related peptide receptor - mouse
C;Species: Mas musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C;Accession: S44203
R;Karperien, M.; van Dijk, T.B.; Hoot-jankers, T.; Cremers, F.; Abou-Samra, A.B.; Boon submitted to the EMBL Data Library, April 1994
A;Pescription: Expression pattern of parathyroid hormone/parathyroid hormone related A;Reference number: S44203
A;Accession: S44203
A;Accession: S44203
A;Status: preliminary
A;Molecule type: mRMA
A;Residues: 1-591 <ARP>
A;Residues: 1-591 <ARP>
A;Cross-references: EMBL:X78936; NID:g474828; PIDN:CAA55536.1; PID:g474829
C;Superfamily: glucagon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change ll-Jan-2000
C; Accession: I59297
R; Accession: I59297
R; Accession: I59297
R; Accession: I59297
R; MulD: 94255468
R; Reference number: I59297; MulD: 94255468
R; Accession: I59297
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C;Superfamily: glucagon receptor
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                                                                                               1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-589 <RES>
A; Cross-references: GB:L34611; NID:g530149; PIDN:AAA40011.1; PID:g530151
C; Genetics:
                                                                                                                           22 ARLDISSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ
  Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 591;
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                                               Indels
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     DB 2;
70.0%; Score 458.5; DB 2; 72.8%; Pred. No. 1.1e-40; ive 10; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%; Score 77; DB 2
32.5%; Pred. No. 4.3;
Live 12; Mismatches
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11.6%; Score 76; DB 2
Best Local Similarity 32.5%; Pred. No. 5.4;
Matches 26; Conservative 12; Mismatches
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Matches 26; Conservative
                                                    Conservative
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                                                                                                                                                                                                                                                                                               SPQGY 125
                                                                                                                                                                                                                                                                                                                                            SP0GY 143
                                                    91;
     Query Match
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                              Best Local
Matches 9
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E;1-21/Domain: signal sequence #status predicted <SIG>
E;2-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;22-41/Product: proadrenomedullin #status predicted <MAT>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C.Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C.Saccession: JNO766; PMO610
R.Sakata, J.: Shimokubo, T.: Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T Biochem. Blophys. Res. Commun. 195, 921-927, 1993
A.Fitle: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv A.Reference number: JNO766; MUID:93384621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-185 <SAK>
A; Residues: 1-185 <SAK>
A; Accession: PN0610
A; Molecule type: protein
A; Molecule type: protein
C; Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom essure control.
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                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19.Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S41600
E;Accession: S41600
E;EBS Lett. 338, 306-310, 1994
A;Tittemura, K; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A;Titte complete amino acid sequence of porcine adrenomedullin and cloning of A;Reference number: S41600; MUID:94139945
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                                                                                                                                               Gaps
                         1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-188 <KIT>
A,Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379
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Pred. No. 1.1e-56;
8; Mismatches 3;
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91.2%;
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Best Local Similarity 91.29
Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       adrenomedullin - pig
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SPQGY 146
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S41600
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Ni Contains: fibrinopeptide B
Ni Contains: fibrinopeptide B
C; Species: Petromyzon marinus (asa lamprey)
C; Date: 25-oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C; Date: 25-oct-1987 #sequence of lamprey fibrinogen beta chain.
A; Recession A25052, MUID:87076582
A; Mocession A25052
A; Molecule type: mRNA
A; Residues: 39-479 - ADGH
A; Residues: 30-479 - ADGH
A; Residues: 37-479 - ADGH
A; Residues: Bibinopen beta chain #status experimental
C; Reywords: blood coagulation; glycoprotein; sulfoprotein
F; 23-477 / Domain: fibrinogen beta/gamma homology <a href="http://domain:fibrinogen beta/gamma">FEGEO-1997 / ADGMINITY FIBRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 VRSEXRLRRADGSW-AWVIDVGQPRFSADGTFLGYVGSVLDITERRAAE-IAQQEAQAFI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 RSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RLDVASEFRKKWNKW-----ALSRGKRELRMSSSYPTGLADV----KAGPAQTLIRPQ 50
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                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                   Length 1051;
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    A;Reference number: A96039; MUID:21368234; PMID:11474104 A;Contents: annotation
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                                                                                                                                                                                                                                                                                                                             63;
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                                                                                                                                                                                                                                                   7,
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                                                                                                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                               Score 75; DB
Pred. No. 13;
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                                                                                                                                                                                                                                           11.5%;
26.9%;
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Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                     A; Genome: plasmid
                                                                                  C;Genetics:
A;Gene: SMa1548
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                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 0.2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
C; Accession: 154195; A42698
R; Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier Renonics 20, 20-26, 1994
A; Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (and rat genomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Crossing Control of the Arabidos of the Control of the Control of the Control of the Control of A; Reference of B:L19475; NID:g467316; PIDN:AAA68098.1; PID:g467317
R;Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A;Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid A;Reference number: A42698; MUID:92212903
A;Accession: A42698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s,
    463 NVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLLP 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                          parathyrold hormone/parathyroid hormone related-peptide receptor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1.585, 'G', 587-591 <ABO>
A; Experimental source: ROS 17/2.8 osteosarcoma cells
A; Note: sequence extracted from NCBI backbone (NCBIP:92187)
C; Superfamily: glucagon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: 154195; MUID:94292182
A; Accession: 154195
                                                                                                                                                            542
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                                                                          50 QDMKGASRSPEDSSPDAARI
                                                                                                                                                    523 ATTNGHSQLPGHAKPGAPAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
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A; Residues: 1-591 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-585, 'G'
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F.1906-2061/Domain: discoidin I amino-terminal homology <DN1>
F.2065-2224/Domain: C2 <DC2>
F.2065-2224/Domain: discoidin I amino-terminal homology <DN2>
F.2065-2224/Domain: discoidin I amino-terminal homology <DN2>
F.2065-2221/Domain: discoidin I amino-terminal homology <DN2>
F.51.55,239,297.460,468.554,741,752,760,776,782,821,938,977,1074,1083,1103,1106,1479,
F.167-193,248-329,500-526,603-684,1725-1751,1907-2061,2066-2221/Disulfide bonds: #sta
F.367-335/Cleavage site: Arg-Asn (protein C) #status predicted
F.363,693,1546/Binding site: alfate (Tyr) (covalent) #status predicted
F.367-377/Cleavage site: Arg-Ser (coaquiation factor Xa) #status absent
F.534-335/Cleavage site: Arg-Ser (coaquiation factor Xa, thrombin) #status experiment
F.1046-1047/Cleavage site: Arg-Ser (thrombin) #status experiment
F.1046-1047/Cleavage site: Arg-Ser (thrombin) #status experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP-binding regulatory protein beta chain - wild oat
C;Species: Avena fatua (wild oat)
C;Species: Avena fatua (wild oat)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 21-Jan-2000
C;Accession: T08036
R;Jones, H.D.; Smith, S.J.; Desikan, R.; Plakidou-Dymock, S.; Lovegrove, A.; Hooley, Plant Cell 10, 245-254, 1998
A;Title: Heterotrimeric G proteins are implicated in gibberellin induction of a-amyla A;Reference number: 216226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,;
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A;Cross-references: EMBL:AF033357; NID:92935697; PIDN:AAC39373.1; PID:92935698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable DNA primase small subunit – fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology F;245-278/Domain: WD repeat homology <WDR>
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   873 DQAAKHRFSWMKLLAHKVGRHLSQDTGSPSGMRPWEDLPSQDTGSPSRMRPWKDPPSDLL 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDKDNVAPRSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSPDAARIRVKRYRQSMNNFQGLRSF--GCRF-----GTCTV--QKLAH--QIYQFTDK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 -----VRTYHGHEGDINSVKFFPDGHRFGTGSDDGTCRLFDMRIRHQLQVYSREPD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPED--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%; Score 71; DB 1; Length 2224; 22.6%; Pred. No. 77; tive 20; Mismatches 52; Indels
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Llarity 23.6%; Pred. No. 18;
Conservative 18; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T08036
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRN-A
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Best Local S
Matches 30
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Matches 2
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A; Residues: 1-857, 'R', 859-864, 'R', 866-924, 'E', 926-1763, 'I', 1765-2212, 'T', 2214-2224 <JEN>
A; Cross-references: GB:MIS657
A; Note: parts of this sequence, including the amino end of the mature protein, were dete
B; Kane, W.H.; Ichinose, A.; Hagen, F.S.; Davie, E.W.
Biochemistry 26, 6508-6514, 1987
A; Title: Cloning of cDNAs coding for the heavy chain region and connecting region of hum
A; Reference number: A27498; MUID:88107560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 48-58;79-89;120-130;191-201;239-249;313-323;368-378;428-437;461-471;533-542;
2070;2111-2120;2172-2181 <CR2.
8:Johny, R.-J.: Pittman, D.D.: Toole, J.J.; Kriz, R.W.; Aldape, R.A.; Hewick, R.M.; Kaufm
Proc. Natl. Acad. Scl. U.S.A. 84, 4846-4850, 1987
A;Title: Complete cDNA and derived amino acid sequence of human factor V.
A;Reference number: A28028; MUID:87260886
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A;Introns: 53/2; 84/1; 125/1; 196/1; 244/1; 318/1; 373/2; 432/3; 466/1; 537/3; 588/1; 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description: acts as a cofactor, with calcium and phospholipid, for the factor Xa prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pathway: blood coagulation

Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidase re

Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidase re

*Reywords: blood coagulation fuplication; glycoprotein; phospholipid binding; plasma;

$1-28/Domain: signal sequence #status predicted <SIG>

$29-737/Product: coagulation factor V #status predicted <MAT>

$29-737/Product: coagulation factor Va heavy chain #status experimental <VAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ferroxidase re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Wolecule type: mRNA
A; Residues: 1188-1215,1315-2224 <KA2>
A; Cross-references: 6B:M14335
A; Note: parts of this sequence were determined by protein sequencing
B; Keller, F.G.; Ortel, T.L.; Quinn-Allen, M.A.; Kane, W.H.
Blochemistry 34, 4118-4114, 1995
A; Reference number: A56139; MuID:95210278
A; Reference number: A56139; MuID:95210278
A; Contents: annotation; thrombin cleavage sites
C; Comment: Factor V is activated by thrombin and partially by coagulain
   N;Alternate names: coagulation labile factor; proaccelerin C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:1574-1905/Domain: A3 <DA3>
F:1581-1905/Domain: ferroxidase repeat homology <FO3>
F:1667-1765/Region: phospholipid binding #status predicted
F:1906-2064/Domain: C1 <DC1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GDB:119896; OMIM:227400
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-2224 <CRI>
A; Cross-references: GB:J05368
A; Accession: A42344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: F5
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IRPQDMKGASRSPEDS----SPDAARIRV---KRYRQSMNNFQGLRSFGCRFGTCTVQK 98
  HQIYQFTDKDKDN-----VAPRSKISPQ 123
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  101
                                             237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 33-328 cBAS>
A; Residues: 33-328 cBAS>
A; Cross-references: GB:MZ7220; NID:g529585; PIDN:AAA41160.1; PID:g529586
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
C; Superfamily: fibrinogen beta chain; liver; plasma
F; 33-65/Domain: fibrinogen disulfide ring homology (fragment) <FDR>
F; 75-324/Domain: fibrinogen beta/gamma homology <FBGS-
F; 75-314/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibrinogen beta chain precursor - rat (fragments)

N;Contains: fibrinopeptide B

N;Contains: fibrinopeptide B

N;Contains: fibrinopeptide B

N;Contains: fibrinopeptide B

C;Species: Ratius norvegicus (Norway rat)

C;Species: Ratius norvegicus (Norway rat)

C;Accession: A0529; PE0010

C;Accession: A0529; PE0010

Proc. Natl. Acad. Sci. U.S.A. 81, 2313-2316, 1984

A;Title: Potential basis for regulation of the coordinately expressed fibrinogen genes: A;Reference number: A93989; MUID:84194000

A;Accession: A05299

A;Molecule type: DNA

A;Residues: 1-32 x FCWA

A;Residues: 1-32 x FCWA

A;Residues: 1-32 x FCWA

A;Residues: 1-32 x FCWA

A;Residues: 1-51 x FCWA

A;Residues: PE0010; MUID:89378771

A;Accession: PE0010; MUID:89378771
           Rigentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1995
A; Reference number: 221815
A; Accession: T39017
A; Accession: T39017
A; Accession: T39017
A; Molecule type: DNA
A; Residues: 1-454
A; Residues: 1-454
A; Cross-references: EMBL: 298531; PIDN: CAB11078.1; GSPDB:GN00066; SPDB: SPAC6B12.10c
C; Genetics:
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 RLDVEVSRHLNHLLKSPPCVHPGTSRVCVPIDIERMDSFNPLK-----VPTVNDLLQE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFG-----TCTVQKLA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 DVASEFRKKW-----NKWA----LSRGKRELRMSSSYPTGLADVKAGPAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RLDVASEFRKKWNKWALSRG-----KRELRMSSSYPTGLADV----KAGPAQTLIRP 49
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20.9%; Pred. No. 18;
+ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                10.5%; Score 69; DB 24.4%; Pred. No. 22; cive 20; Mismatches
                                                                                                                                                                                                                                                                                                                   C; Superfamily: DNA primase 50K chain
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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L----DKNSQN 390
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C; Accession: T39017
                                                                                                                                                                                                                                                                             A; Map position: 1
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hypothetical protein F28B23.2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: H86389
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallo A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                       protein F56B3.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: F88632
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: F88632
A;Note: barnata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Residues: 1-926 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:chr_IV; PIDN:AAC02615.1; PID:92854201; GSPDB:GN00022; CESP:F56 C;Genetics:
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A;Gross-references: GB:AE005172; NID:g11079511; PIDN:AAG29222.1; GSPDB:GN00141
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : | : | : | : | OAPP-----TKVVEEMANELEVLEEYGNREDQEKYNRLATVFWKIID 654
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24.0%; Pred. No. 72;
ive 19; Mismatches
| | | : | : | : | HOME | | | : | : | HOME | 
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Best Local Similarity 24.0
Matches 30; Conservative
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Best Local Similarity
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A; Wolecule type: DNA
A; Residues: 1095-3144 <WED>
A; Residues: 1095-3144 <WED>
A; Cross-references: EWEL2/3145; MIPS:YLL040c
A; Cross-references: Extrain S288C
B; Lombardo, A.; Carine, K.; Scheffler, I.E.
B; Lombardo, A.; Carine, K.; Scheffler, I.E.
A; Blol. Chem. 265, 10419-10423, 1990
A; Title: Cloning and characterization of the iron-sulfur subunit gene of succinate dehych A; Reference number: A35435; MUID:90285165
A; Accession: S14891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                             VPSI3 protein - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein L0901; protein YLL040c
C;Species: Saccharomyces cerevisiae
C;Species: Ol-Aug-1995 #sequence_revision 24-May-1996 #text_change 13-Sep-1998
C;Accession: S64791; S64792; S14891
R;Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D. A;Reference number: S64775
A;Reference number: S64775
A;Recession: S64779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1354 SGGKGEIKSPSPDPASL---SSESERTATPQSIQGSNKSNIKNPEQKYLDFSFKAPKIA 1409
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71 VKRYRQ-----SMNN-----FQGLRSFGCRFG---TCTVQKLAHQIYQFTDKD----K 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 SRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRS----PE----DSSPDAARIR 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: involved in regulation of membrane traffic C;Reywords: transmembrane protein F;1084-1100/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Rosidues: 1-1360 < DUE>
A; Cross-references: EMBL:Z73145; MIPS:YLL040c
A; Experimental source: Strain S288C
R; Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SGD:VPS13; VPT2; SOI1
A;Cross-references: SGD:SO003963; MIPS:YLL040c
A;Map position: 12L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: October 17, 2002, 15:22:40 Job time : 13.8078 secs
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A; Residues: 2991-3047, 'L' <LOM>
A; Cross-references: EMBL:J05487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: translation not shown
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1466 DNKHTELIPKSK 1477
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October 17, 2002, 15:20:12; Search time 21.5798 Seconds (without alignments) 643.390 Million cell updates/sec
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| SIDSI/gcgdata/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqp/eneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqp/eneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqp/eneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqp/eneseqp-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseqp/eneseqp-embl/AA1991.DAT:*
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| SIDSI/gcgdata/geneseqp-embl/AA1991.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747574 seqs, 111073796 residues
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Listing first 45 summaries
                                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human adrenomeduli	Human adrenomedull	Porcine adrenomedu	Porcine adrenomedu	Rat adrenomedulin	Rat adrenomedullin	Human secreted pro	UspA(1-57)-(A)-(GS	UspA(1-84)-(GS	UspA(1-56)-(DD)-(G	Human adrenomedull
SUMMARIES	AAB49697	AAB60344	AAB49698	AAB60345	AAB49699	AAB60346	AAG00251	AAB75122	AAB75124	AAB75123	AAB75110
DB	22	22	22	22	22	22	21	22	22	22	22
% Query Match Length DB	185	185	188	188	185	185	97	120	147	120	52
% Query Match	100.0	100.0	93.3	93.3	70.0	70.0	58.6	45.7	44.6	44.5	43.2
Score	655	655	611	611	458.5	458.5	384	299.5	292	291.5	283
Result No.	-	7	m	4	S	9	7	œ	6	10	11

Composition for promoting passive elongation of vesicle smooth muscle comprises adrenomedulin $\,$

Adrenomedullin pep	Human adrenomeduli	Glycine extended h	Glycine extended a	Linker peptide-adr	Thioredoxin-(GSGSG	Adrenomedullin pep	Rat adrenomedullin	Adrenomedullin pep	Adrenomedullin pep	Adrenomedullin pep	Adrenomedullin pep	Human preproadreno	Adrenomedullin pep	Human adrenomeduli	Human proadrenomed	Adrenomedullin pep	Adrenomedullin pep	A mutant parathyro	Tethered PTH-1 rec	Rat bone PTH/PTHrP	Rat bone PTH/PTHrP	Parathyroid hormon	Human Factor V. H	Human lipoprotein	Novel human diagno	Propionibacterium	C glutamicum prote	Human protein SEQ	A human regulator	Human protein SEQ	human	Novel human diagno	human
	AAE09818	AAB75111	AAB75112	AAB75113	AAB75114	AAB91763	AAE09819	AAB91765	AAB91767	AAB91768	AAB91761	AAW25160	AAB91762	AAE09827	AAW25161	AAB91766	AAB91769	AAB07529	AAY96983	AAR27706	AAR92277	AAW73316	AAW04254	AAY49564	ABG05508	AAU62051	AAG91263	AAM79810	AAB18668		ABG19073	ABG08359	ABG02404
22	22	22	22	22	22	22	22	22	22	22	22	18	22	22	18	22	22	21	21	13	17	20	17	20	22	22	22	22	21	22	22	22	22
52	52	53	53	62	170	48	20	52	53	40	37	31	31	31	20	20	20	435	446	591	591	591	2224	2224	185	343	783	401	462	462	515	651	944
43.2	43.2		43.2	٠.				34.	33.	29.	27	24	24	24	16.	15.	14.	11.	11	11.	11	11.	10.	10.	10	10.	10.				10.4	10.4	10.4
283	283	283	283	283	283	239	231	227	219.5	196	181.5	163	163	163	107	104	97	75	75	75	75	75	71	71	70.5	70	69	æ,	68.5	ä	68	68	89
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

RESULT 1 AAB49697 ID AAB XX AAC AAB XX AAC AAB XX BDT 04- XX BDT 08- XX BDS HOM XX HOM XX HOM XX BD 28- YX Z 23- YX Z 23- YX Z 3- YX Z X Z X X X X X X X X X X X X X X X X	RESULT 1 AAB49697 standard; Protein; 185 AA. XX X
2	WFL; ZUUL-U8U/24/U9. N-PSDB; AAF29138.
PT XX PS	Composition for promoting passive elongation of vesicle smooth comprises adrenomedulin - Claim 1; Page 26-27; 42pp; Japanese.

ALIGNMENTS

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represents human adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI: 2001-080754/09.
                                                       Similarity
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                      185 AA;
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                                                                                                                                                                                   121 SPQGY 125
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                      Sequence
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                                            Query Match
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         This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary alsorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the human adrenomedulin protein, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                           DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                              Gaps
                                                                                                                                                                                               The invention relates to a composition containing adrenomedullin for
                                                                                                                                                                                   1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                            ;
0
                                                                                                                                   Length 185;
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                                                                                                                                   : Score 655; DB 22;
: Pred. No. 1.8e-69;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                           AAB60344 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             Human adrenomedullin precursor.
                                                                                                                                     100.08;
                                                                                         composition of the invention
                                                                                                                                              100.08;
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21-MAR-2000; 2000JP-0079171.
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                          Conservative
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                                                                                                                                                 Similarity
                                                                                                              185 AA;
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Matches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for releving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the porcine adrenomedulin protein, which is used in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                  61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVRAGPAQTLIRPQDMKGASRSPE 60
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                                                            Gaps
                                                                                                                                                 22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE
                                                                                                                1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; procine.
   Length 185;
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Local Similarity 91.2%; Pred. No. 3.1e-64;
nes 114; Conservative 8; Mismatches 3;
                                                            ö
   655; DB 22;
No. 1.8e-69;
                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine adrenomedulin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 31-33; 42pp; Japanese.
         Score
                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB49698 standard; Protein; 188 AA.
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHIO ) SHIONOGI & CO LTD
                                    Best Local Similarity 100.
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises adrenomedulin
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142 SPQGY 146

(first entry)

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AAB49699 standard; Protein; 185 AA.
                                                                                             04-APR-2001
                                                                          AAB49699;
                                            AAB49699
                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorthoea. The present sequence represents porcine adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                           Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                         Porcine; pig; adrenomedullin; precursor; bradykinin antagonist; uterine contraction inhibitor; premature birth; miscarriage; abortion; dysmenorrhoea; obstetric; gynaecological.
                               DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to a composition containing adrenomedullin for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ
                    DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 611; DB 22;
Pred. No. 3.1e-64;
8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 43-44; 54pp; Japanese.
                                                                                                                            AAB60345 standard; Protein; 188 AA.
                                                                                                                                                                                     Porcine adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.3%;
91.2%;
                                                                                                                                                                                                                                                                                                                              99JP-0177548.
2000JP-0079171.
                                                                                                                                                                                                                                                                                                        23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                           (SHIO ) SHIONOGI & CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-080755/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAF27229
                                                          SPQGY 125
                                                                              SPQGY 146
                                                                                                                                                                                                                                                                WO200078339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPQGY 125
                                                                                                                                                                                                                                                                                                                             23-JUN-1999;
21-MAR-2000;
                                                                                                                                                                  06-APR-2001
                                                                                                                                                                                                                                                                                     28-DEC-2000
                                                                                                                                                                                                                                                Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                              Yanagita T;
                                                                                                                                                 AAB60345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
 22
                    61
                                                           121
                                                                             142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ARLDISSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                             Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.0%; Score 458.5; DB 22; 72.8%; Pred. No. 3.7e-46; ive 10; Mismatches 2.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 37-38; 42pp; Japanese.
Rat adrenomedulin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60346 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                             99JP-0177549.
                                                                                                                                                                                                                                                           23-JUN-2000; 2000WO-JP04166.
                                                                                                                                                                                                                                                                                                                                                          (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.03
Best Local Similarity 72.85
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises adrenomedulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-080754/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 AA;
                                                                                                                 Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF29140
                                                                                                                                                                WO200078338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPQGY 143
                                                                                                                                                                                                                                                                                                           23-JUN-1999;
                                                                                                                                                                                                                28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                          Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60346;
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The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length consone mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.6%; Score 384; DB 21;
100.0%; Pred. No. 1.1e-37;
ive 0; Mismatches 0;
                                                                                                                                                                                               Glordano J;
                                                                                                                                                                                                                                                                                                                                                                            Claim 13; SEQ ID 4332; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB75122 standard; Protein; 120 AA.
                                                                                                                                                                                                 Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-0CT-2000; 2000WO-JP07023
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                                                                           21-FEB-2000; 2000EP-0200610.
                                                                                                                  99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DSSPDAARIRVKRYR
                                                                                                                                                                                                                                     WPI; 2000-500381/45.
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Best Local Similarity
Matches 75; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 AA;
                                                                                                                                                                                                                                                          N-PSDB; AAC00257
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                                                                                                                                                          (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1999;
                                                                                                                  26-FEB-1999;
EP1033401-A2
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                                   06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB75122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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AAB75122
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;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorshoea. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for inhibiting automatic uterine contraction or contraction
                                                            adrenomedullin; precursor; bradykinin antagonist; ine contraction inhibitor; premature birth; miscarriage; abortion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 ARLDISSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.0%; Score 458.5; DB 22; Length 185; 72.8%; Pred. No. 3.7e-46; tive 10; Mismatches 21; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caused by bradykinin comprises adrenomedullin
                                                                                                      dysmenorrhoea; obstetric; gynaecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein, SEQ ID NO: 4332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 48-49; 54pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG00251 standard; Protein; 97 AA.
                      Rat adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                   23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                              23-JUN-2000; 2000WO-JP04167
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Best Local Similarity 72.8%
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                                                                                                                                                                                                                                                                                                                                                                (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-080755/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 AA;
                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAF27230
                                                                                                                                                                                 WO200078339-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPQGY 143
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                                                                                                                                                                                                                        28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                         Yanagita T;
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                                                                                   uterine
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Gaps

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Length 97; Indels

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WPI; 2001-282044/29.
N-PSDB; AAH19865.
                                                                                                                                                                                                                                                                                                                             Local Similarity
les 65; Conserv
                                                                                                                                                                                                                                                                    147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-2001
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                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB75123;
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4,
                                                                                                                                                                                                                                                                          The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                          Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adrenomedullin; glycine extended adrenomedullin; AM: AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 DVNYSDLY-TGLIDVNLG------DMAGS------GSGDAF-----EYRQSMNNFQG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2/;
12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 299.5; DB 22;
Pred. No. 1.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.56
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                         Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                      Claim 17; Page 68; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB75124 standard; Protein; 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.78;
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                   (SHIO ) SHIONOGI & CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66; Conservative
                                                         Takimoto A, Mitsuda Y,
                                                                                               WPI; 2001-282044/29
N-PSDB; AAH19864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-282044/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH19866.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                 The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDS-----SPDAARIRV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 KRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 -EYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.6%; Score 292; DB 22; 57.0%; Pred. No. 1.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakayama T,
Claim 17; Page 71; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB75123 standard; Protein; 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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52 AA.

(first entry)

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AAB91759 standard; Peptide;
                                                                      22-JUN-2001
                                                                                                                                                                                                                                                17-MAY-1999;
                                                                                                                                                                                                        23-NOV-2000
                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                  AAB91759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
           RESULT 12
                     AAB91759
                                        δλ
                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell: (b) restricted digestion of the fused protein by a protease followed by collection of sediment: and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                             Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host \, -
                                                              Gaps
                                                                                 24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 83
                                                                                               39 DVNYSDLY-TGLIDVNLG------DDDGS------GSGDAF-----EYRQSMNNFQG 77
                                                             21;
                                        DB 22; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 52;
                                                             13; Indels
                                                                                                                         84 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                                    Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 283; DB 22;
Pred. No. 4.5e-26;
); Mismatches 0;
                                                  Pred. No. 1.3e-26;
                                                            3; Mismatches
                                        Score 291.5;
exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Takimoto A, Mitsuda Y, Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75pp; Japanese.
                                                                                                                                                                                                                                                         Human adrenomedullin (AM) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.2%; Scor
100.0%; Pre
0; }
                                                                                                                                                                                              AAB75110 standard; Protein; 52 AA
                                      44.5%;
                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                          99JP-0294147.
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              (SHIO ) SHIONOGI & CO LTD
                                                             65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-282044/29.
N-PSDB; AAH19806.
                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                     120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 AA;
                                                                                                                                                                                                                                                                                                                               WO200127310-A1.
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1999;
                                                                                                                                                                                                                                      31-JUL-2001
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                     Seguence
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                                                                                                                                                                                                                  AAB75110;
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AAB75110
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The present invention describes a modified therapeutic peptide (I) comparising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and malelmido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptides stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various dissorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body woodifying therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
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                                                             Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Preu. ...
Adrenomedullin peptide (AM) SEQ ID NO:935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 498; 733pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0134406.
99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bridon DP, Ezrin AM,
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Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                 WO200069900-A2.
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-SEP-1999;
15-OCT-1999;
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AAE09818 standard; peptide; 52 AA.

RESULT 13 AAE09818

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Gaps

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Indels

Conservative

52;

Matches

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AAE09818;

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adrehomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75124 represent sequences which are used in the
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                                                                                                                                                                                                                                                     Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
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                                                                                                            Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method (M1) for
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4.6e-26;
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100.0%; Pred. No. . . .
0; Mismatches
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                                                                                                            Nakayama T,
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                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 46; 75pp; Japanese.
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99JP-0294147.
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                                                         (SHIO ) SHIONOGI & CO LTD
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nes 52; Conservative
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                                                                                                                Mitsuda Y,
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N-PSDB; AAH19808.
                                                                                                                                                                      2001-282044/29.
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Synthetic.
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15-OCT-1999;
                                                                                                                Takimoto A,
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AAB75112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antagonists of the vasoactive peptide calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro of in assays to identify and/or isolate CGRP receptors or with intect binding to its receptor. The present sequence is human adrenomedullin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                                                                                      Human; vasoactive peptide; calcitonin gene related peptide; CGRP; CGRP-receptor identification; adrenomedullin.
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Pred. No. 4.5e-26;
0; Mismatches 0;
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100.0%; Pre
0;
                                                                                                            Human adrenomedullin peptide #1.
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                                                         (first entry)
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les 52; Conserv
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Query Match Best Local S Sequence

Matches

AAB75111;

RESULT 14 AAB7511

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Gaps

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producing

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The present invention describes a method (MI) for producing darenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment: and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                   Query Match
43.2%; Score 283; DB 22; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.6e-26;
Matches 52; Conservative 0; Mismatches 0; Indels
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Search completed: October 17, 2002, 15:21:13 Job time : 22.5798 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

October 17, 2002, 14:45:21; Search time 2.39401 Seconds (without alignments) 646.939 Million cell updates/sec Run on:

US-10-018-924-2_COPY_107_146
219
1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		P35318 homo sapien	s sns	77559 cani	062827 bos taurus		P97297 mus musculu	Q63120 rattus norv		_			O15439 homo sapien		Q04604 rana nigrom	_			O15438 homo sapien		P34427 caenorhabdi	P58492 yersinia pe	xenopus 1	026346 methanobact	P30419 homo sapien	0	P31717 bos taurus	P04409 bos taurus	P17252 homo sapien	P20444 mus musculu	P10102 oryctolagus	569	P52087 pseudomonas	~
SUMMARIES	ID		ADML_PIG	ADML_CANFA	ADML_BOVIN	ADML_RAT	ADML_MOUSE	MRP2_RAT	MRP2_HUMAN	MRP2_RABIT	SLS6_BRAOL	VG48_BPMU	MRP4_HUMAN	G33_RAT	TYRO_RANNI	Y4KA_RHISN	SLS2_BRAOA	DNAB_RHOMR	MRP3_HUMAN	INXB_CAEEL	LI36_CAEEL	ZIPA_YERPE	PPAS_XENLA	SYH_METTH	NMT1_HUMAN	- 1	- 1	KPCA_BOVIN	KPCA_HUMAN	KPCA_MOUSE	KPCA_RABIT	KPCA_RAT	UVRA_PSELE	AT5C_HUMAN
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df	Query Match		97.3	95.0	92.5	89.2	85.4	27.9	26.9	25.1	24.9	23,3	23.3	23.1	23.1	22.6	22.4	22.4	22.4	22.1	22.1	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	;	1.
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P56869 chiamydia m 09290 chlamydia t 084317 chlamydia t 000341 homo sapien P38808 saccharomyc 024317 drosophila 008410 coturnix co 09f415 mycobacteri P5715 buchnera ap P53049 saccharomyc P16144 homo sapien 007815 neisseria m
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RPOB_CHLMU RPOB_CHLPN RPOB_CHLTR RVGLN_HUMAN YHP5_YEAST PRII_DROME TYRO_COTJA RECA_MYCFV FLIF_BUCAI FLIF_BUCAI TITB4_HUMAN RS18_HUMAN
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ALIGNMENTS

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rissue-Adrenal medulla;
SEQUENCE OF 22-41
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Matches
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                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                  PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES WINHBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASKA, VOLUME, ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
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                                                                                                                   SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94139945; PubMed-8043068; Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.; "Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encoding its precursor."; PEBS Lett. 338:306-310(1994).
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Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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  INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
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                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
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16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 34, Last annotation update)
17-OCT-2001 (Rel. 34, Last annotation update)
18-OCT-2001 (Rel. 34, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADRENOMEDULLIN
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0; Mismatches
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Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
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EMBL; S73906; AAC60642.1; -.
EMBL; D43639; BAA07756.1; ALT_SEQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JN0476; JN0476.
PIR; JN0684; JN0684.
PIR; JC2351; JC2351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone; Amidation;
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Matches 40; Conserv
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P53366;
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MOD_RES
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                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
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077559; 09VC9;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM Precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-2C terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BT SIMILARITY.
AMIDATION (G-142 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
71749460F5660461 CRC64;
                    Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y., Kawamoto M., Minamino N., Matsuo H., Eto T.; Karamoto M., Minamino N., Matsuo H., Eto T.; Allorition and hypotensive activity of proadrenomedullin N-terminal 20 peptide (PAMP)."; FEBS Lett. 351:35-37(1994).
--- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
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MEDLINE-99002704; PubMed-9788655;
Ono Y., Kojima M., Okada K., Kangawa K.;
"CDNA cloning of canine adrenomedullin and its gene expression in heart and blood vessels in endotoxin shock.";
Shock 10:243-247(1998).
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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"Cloning of cDNA encoding canine adrenomedullin.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                 -I- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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1.9e-22;
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Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Secreted
MEDLINE-94357274; PubMed-8076689;
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97.58;
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                     PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
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16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barker S., Wood E., Clark A.J.L., Corder R.; "Cloning of bovine preproadrenomedullin and inhibition of its basal expression in vascular endothelial cells by staurosporine."; Life Sci. 62:1407-1415(1988).
FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
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AMIDATION (G-147 PROVIDE AMIDE GROUP)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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809D6A64F98F5578 CRC64;
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                      SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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EMBL; U96127; AAD09957.1; -.
InterPro; IPR001710; Adrenomedullin.
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95.0%;
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Best Local Similarity
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16-OCT-2001
16-OCT-2001
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and biological activities of rat adrenomedullin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
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Sciurognathi; Muridae; Murinae; Rattus
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(BY SIMILARITY)
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BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
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Matsuo H., Eto T.;
                                                                                                                                                                                                                   BY SIMILARITY.
ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 188;
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 202; DB 1; Leng
bred. No. 6.4e-21;
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                                                                            EMBL; AJ001613; CAA04866.1; -.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
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MEDLINE=96102137; PubMed=8524787;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                           92.2%;
92.5%;
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Best Local Similarity 92.5
Matches 37; Conservative
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                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  in no
                                                                                                                                                                                                                         BY SIMILARITY.
PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
BY SIMILARITY.
ADRENOMEDULLIN.
PREPROAM C.TERMINAL FRAGMENT (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells at the implantation site."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; Genomic organization, expression, and chromosomal mapping of the mouse adrenomedullin gene"; Genomics 37:395-399(1996).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
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Yotsumoto S., Ko M.S.H.;
"Expression of mouse adrenomedullin gene in trophoblastic giant
                                                                                                                                                                                                      Hormone, Amidation, Cleavage on pair of basic residues, Signal.
SIGNAL
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BY SIMILARITY.
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  non-profit institutions as long as its content is
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                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
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                                                                                                                                         Interpro; IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
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MEDLINE-97092892; PubMed-8938454;
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87.5%;
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185
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Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "" reference of the hepatocyte canalicular isoform of the multidrug resistance protein, cMrp, reveals a novel conjugate export pump deficient in hyperbilirubinemic mutant rats."; J. Biol. Chem. 271:15091-15098(1996).
                                                                                                                                                                                                                                                                      PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Canalicular multispecific organic anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance
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AMIDATION (G-145 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
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MEDLINE-96180672; PubMed-8599091;
Paulusma C.C., Bosma P.J., Zaman G.J.R., Bakker C.T.M., Otter M., Scheffer G.L., Scheper R.J., Borst P., Oude Elferink R.P.J.;
"Congenital jaundice in rats with a mutation in a multidrug resistance-associated protein gene.";
Science 271:1126-1128(1996).
                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARÍTY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                 Pflucer: PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
Hormone; Amidation; Cleavage on pair of basic residues; Signal.
stgnar.
1 21 BY SIMILARITY.
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PREPROAM C-TERMINAL FRAGMENT
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C88C99045A79C898 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 187; DB 1;
Pred. No. 7.5e-19;
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2; Mismatches
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InterPro; IPR001710; Adrenomedullin.
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MEDLINE-96279006; Pubmed-8662992;
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                                                                           EMBL; D78349; BAA11367.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 85.4%;
Local Similarity 85.0%;
Les 34; Conservative
                                                                                                    AAB36535.1;
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15-JUL-1998 (Re.
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D5FB55571BFDDB39 CRC64;

173383 MW;

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SEQUENCE
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MRP2_HUMAN
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                 HYPERBILIRUBINEMIA (EHBR).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                     SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
DISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF HEREDITARY CONJUGATED
          Int. Hepatol. Commun. 292:292-299(1996).
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CYTOPLASMIC (BY SIMILARITY).
2 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
3 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                Transmembrane; Transport; Repeat. EXTRACELLULAR (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).

17 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

ATP (POTENTIAL).
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defective in Eisai hyperbilirubinemic rats (EHBR).";
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N-LINKED (GLCNAC. . .)
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N-LINKED (GLCNAC. . .)
M -> V (IN REF. 3).
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EMBL; X96393; CAA65257.1; -.
EMBL; D86086; BAA13016.1; -.
HSSP; P13569; 1NBD.
InterPro; IPR001553; AAA.
InterPro; IPR001140; ABC_transporter_tmem.
InterPro; IPR001494; ARC_transporter_tmem.
InterPro; IPR001687; ATP_GTP_A.
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Pfam; PF00005; ABC_tran; 2.
SWART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER;
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MEDLINE-98087571; PubMed=9425227;
Wada M., Toh S., Taniguchi K., Nakamura T., Uchiumi T., Kohno K.,
Yoshida I., Kimura A., Sakisaka S., Adachi Y., Kuwano M.;
"Mutations in the canilicular multispecific organic anion transporter
(CMOAT) gene, a novel ABC transporter, in patients with
hyperbilirubinemia II/Pubin-Johnson syndrome.";
Hum. Mol. Genet. 7:203-207(1998).
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Kool M., de Haas M., Ponne N.J., Paulusma C.C., Oude-Elferink R.P.J.,

Baas F., Borst P.;
                                                                          Gaps
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MEDLINE=96590592; PubMed=8797578;
Taniguchi K., Wada M., Kohno K., Nakamura T., Kawabe T., Kawakami M., Ragotani K., Okumura K., Akiyama S., Kuwano M.;
"A human canalicular multispecific organic anion transporter (CMOAT) gene is overexpressed in cisplatin-resistant human cancer cell lines with decreased drug accumulation.";
Cancer Res. 56:4124-4129(1996).
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MEDLINE=96279006; PubMed=8662992;
Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
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                                                                                                                                                                                                                                                                                                                                                                   MRP2_HUMAN STANDARD; PRT; 1545 AA.
092887; 09963; 092798; 014022; 092500; 09UMS2;
15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Canalicular multispecific organic anion transporter 1 (Multidrug resistance associated protein 2) (Canalicular multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resistance protein, cMrp, reveals a novel conjugate export pump deficient in hyperbilirubinemic mutant rats."; J. Biol. Chem. 271:15091-15098(1996).
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MEDLINE-99162196; PubMed-10053008;
Toh S., Wada M., Uchiumi T., Inokuchi A., Makino Y., Horie Y.,
       DB 1; Length 1541;
                                                                          Indels
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                               Pred. No. 2.2;
4; Mismatches
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       Score 61;
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   27.9%;
38.2%;
Query Match 27.9
Best Local Similarity 38.2
Matches 13; Conservative
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PROSITE; PSÓ0211; ABC_TRANSPORTER; 1.
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
Disease mutation.
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InterPro: IPR001140; ABC transporter_tmem.
InterPro: IPR003439; ABC_transportr.
InterPro: IPR001687; ATP_GTP_A.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
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AJ132287; CAB45309.1; --
AJ132289; CAB45309.1; JOINED.
AJ132289; CAB45309.1; JOINED.
AJ132289; CAB45309.1; JOINED.
AJ132291; CAB45309.1; JOINED.
AJ132292; CAB45309.1; JOINED.
AJ132294; CAB45309.1; JOINED.
AJ132295; CAB45309.1; JOINED.
AJ132295; CAB45309.1; JOINED.
AJ132295; CAB45309.1; JOINED.
AJ132296; CAB45309.1; JOINED.
AJ132299; CAB45309.1; JOINED.
AJ132309; CAB45309.1; JOINED.
AJ132309; CAB45309.1; JOINED.
AJ132301; CAB45309.1; JOINED.
AJ132301; CAB45309.1; JOINED.
AJ132305; CAB45309.1; JOINED.
AJ132305; CAB45309.1; JOINED.
AJ132306; CAB45309.1; JOINED.
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AU132200, CAB45309.1; JG
AU132301, CAB45309.1; JG
AU132302, CAB45309.1; JG
AU132304, CAB45309.1; JG
AU132304, CAB45309.1; JG
AU132305, CAB45309.1; JG
AU132305, CAB45309.1; JG
AU132306, CAB45309.1; JG
AU132309, CAB45309.1; JG
AU132310; CAB45309.1; JG
AU132310; CAB45309.1; JG
AU132310; CAB45309.1; JG
AU132311; CAB45309.1; JG
AU132312, CAB45309.1; JG
AU132313; CAB45309.1; JG
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30-MAY-2000 (Rel. 39, Last sequence update)
16-CTT-2001 (Rel. 40, Last annotation update)
16-CTT-2001 (Rel. 40, Contains anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance protein) (Epithelial basolateral chloride conductance regulator).
ABCC2 OR MRP2 OR EBCR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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EXTRACELLULAR (BY SIMILARITY).

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CYTOPLASMIC (BY SIMILARITY).

12 (BY SIMILARITY).

13 (BY SIMILARITY).

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EXTRACELULAR (BY SIMILARITY).
3 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
4 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
5 (BY SIMILARITY).
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EXTRACELLULAR (BY SIMILARITY).

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CYTOPLASMIC (BY SIMILARITY).
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Pred. No. 4.2;
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17 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
ATP (POTENTIAL).
ATP (POTENTIAL).
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CYTOPLASMIC (BY SIMILARITY).
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                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                       van Kuijck M.A., van Aubel R.A.M.H., Busch A.E., Lang F., Russel F.G.M., Bindels R.J.M., van Os C.H., Deen P.M.T.; "Molecular Coloning and expression of a cyclic AMP-activated chloride conductance regulator: a novel ATP-binding cassette transporter."; Proc. Natl. Acad. Sci. U.S.A. 93:5401-5406(1996).
                                                                                                                                             by
in
                                                                                                                                                                                                    -i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                                                                                 -!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
                                                                                                                      van Aubel R.A.M.H., van Kuijck M.A., Koenderink J.B., Deen P.M.T.,
van Os C.H., Russel F.G.M.;
                                                                                                                                         "Adenosine triphosphate-dependent transport of anionic conjugates the rabbit multidrug resistance-associated protein Mrp2 expressed
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3 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).
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1 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
14 (BY SIMILARITY).
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InterPro: IPR001140; ABC_transporter_tmem.
InterPro: IPR001499; ABC_transportr.
InterPro: IPR001687; ATP_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                PS00211; ABC_TRANSPORTER; 1
                                                                                                                                                                       Mol. Pharmacol. 53:1062-1067(1998)
                                                                                                             MEDLINE=98279125; PubMed=9614209;
                             MEDLINE=96224297; PubMed=8643587;
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Pfam; PF00005; ABC_tran; 2.
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          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
Nature 326:523-523(1987).
-!- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
(THE INABILITY OF FLOWENING PLANTS TO ACHIEVE SELF-FERTILIZATION).
-!- TISSUE SPECIFICITY: STICMA.
-!- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.; "Amino-acid sequence of glycoproteins encoded by three alleles of the S locus of Brassica oleracea."; Nature 326:617-619(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                           Gaps
15 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

16 (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).

17 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

ATP (POTEWITAL).

ATP (POTEWITAL).

ATP (BOTEWITAL).

N-LINKED (GLCNAC. ..) (POTEWITAL).

N-LINKED (GLCNAC. ..) (POTEWITAL).

N-LINKED (GLCNAC. ...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.OLERACEA.
-!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                             DB 1; Length 1564;
                                                                                                                                                                                                                                                 NKED (GLCNAC. . .) (POTE
D8FBF5AC8FE45873 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-locus-specific glycoprotein S6 precursor (SLSG-6).
                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                1481 FSHCTVITIAHRLHTIMDSDKIMVLDNGNIVEYG 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 AA
                                                                                                                                                                                                                                                                                                                                   Pred. No. 15;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y00268; CAA68375.1; -. EMBL; X03170; CAA26934.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea (Cauliflower).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A27827; A27827.
InterPro; IPR001480; B_lectin.
InterPro; IPR003609; Pan_app.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                           25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KINASE RECEPTOR (ZMPK1).
                                                                                                                                                                                                                                                               175542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 318:263-267(1985).
                                                                                                                                                                                                                                                                                                                                                           Conservative
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1232
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1564 AA;
                                                                                                                                                                                                                                                                                                                                   Similarity
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NP_BIND
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                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Morgan G., Hatfull G., Hendrix R.;
Morgan G., Hatfull G., Hendrix R.;
Genome of bacteriophage Mu and comparison with the Haemophilus
influenzae Mu-like prophage FluMu.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: SOME, TO H.INFLUENZAE HI1521 AND SOME, TO E.COLI YMFQ.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                    N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                            14; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBI_TaxID=10677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                      Length 436;
                                                                             S-LOCUS-SPECIFIC GLYCOPROTEIN
                                                                                                                                                                                                                                             227 GVRFSGIPEDQKLSYMVYNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.3%; Score 51; DB 1; Length 180; 50.0%; Pred. No. 5.8;
                                                                                                                                                                                                                                 3 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 40
                                                       Glycoprotein; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF083977; AAF01126.1; -.
SEQUENCE 180 AA; 20468 MW; 3045A6C185B48BF9 CRC64;
                                                                                                                                                                                       DB 1;
                                                                                                                                                                             24.9%; Scor.
28.6%; Pred. No. 4..,
10; Mismatches
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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InterPro; IPR000858; Slocus_glycop.
Pfam; PF01453; Agglutinin; 1.
Pfam; PF00954; S_locus_glycop; 1.
SMART; SM00108; B_lectin; 1.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRP4_HUMAN STANDARD; F 015439; Q9Y6J2; 15-7UL-1998 (Rel. 36, Created) 16-OCT-2001 (Rel. 40, Last sequile-OCT-2001 (Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 CTVQKL--AHQIYQFTDKDKDN 28
                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                               49779 MW;
                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
                                                      Self-incompatibility;
                                                                                                                                                                  436 AA;
                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage Mu.
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                                                                 SIGNAL
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MRP4_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- TISSUE SPECIFICIATY: WIDELY EXPRESSED, WITH PARTICULARLY HIGH
LEVELS IN PROSTATE, BUT IS BARELY DETECTABLE IN LIVER.
-:- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kool M., de Haas M., Scheffer G.L., Scheper R.J., van Eijk M.J., Juijn J.A., Baas E., Borst P.; "Analysis of expression of cMOAT (WRP2), MRP3, MRP4, and MRP5, homologues of the multidrug resistance-associated protein gene (MRP1), in human cancer cell lines."; Cancer Res. 57:3537-3547(1997).
Multidrug resistance-associated protein 4 (MRP/cMOAT-related ABC transporter) (MOAT-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                        MEDLINE-98324262; PubMed-9661885;

Lee K., Belinsky M.G., Bell D.W., Testa J.R., Kruh G.D.;

"Isolation of MoAr-B, a widely expressed multidrug resistance-

associated protein/canalicular multispecific organic anion

transporter-related transporter.";

Cancer Res. 58:2741-2747(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Transmembrane; Transport; Repeat. 93 113 POTENTIAL.
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InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; APE_GTP_A.
Pfam; PF00005; ABC_tran; 2.
Pfam; PF00064; ABC_membrane; 2.
SWART; SW00382; AAA; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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MEDLINE-97413640; PubMed-9270026;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1155-1316 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF071202; AAC27076.1; -. EMBL; U83660; AAB11757.1; -. HSSP; P13569; 1NBD. MIM; 605250; -.
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=9606;
                             transporter) (
ABCC4 OR MRP4.
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ATP-binding;
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                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                         Chrapkiewicz N.B., Davis C.M., Chu D.T.W., Granner D.K.; "Rat gene 33: analysis of its structure, messenger RNA and basal promoter activity.";
 . .) (POTENTIAL) . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 459;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
WEDLINE-89138017; Pubmed-3224831;
Tindal M.H., Lee K.L., Isham K.R., Cadilla C., Kenney F.T.;
"Structure of a multihormonally regulated rat gene.";
                                                                                                                                                                                                                                                                                                                                                                                                              Gene 71:413-420(1988).
-1- INDUCTION: BY CAMP, GLUCOCORTICOIDS, PHORBOL ESTERS AND
                                               DB 1; Length 1325; 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                       Indels
                    > D (IN REF. 2).
9C5750A748BB96CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      459 AA; 49941 MW; EBD90F11757AC549 CRC64;
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 N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                 01-NoV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Gene 33 polypeptide.
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                                                                                                                                                                459 AA.
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                                                                       4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50.5;
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                                                  Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 17:6651-6667(1989)
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                                                                                                                                                                                                                                                                                                 MEDLINE=89385990; PubMed=2780291;
                             1325 AA; 149539 MW;
                                                                                                              1222 KFAHCTVLTIAHRLNTIIDSDK 1243
                                                                                      5 RFGTCTVQKLAHQIYQFTDKDK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 004604;
01-0CT-1993 (Rel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.1%;
32.4%;
                                                   23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB08828.1; -
                                                           40.98;
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
 1176
1309
1302
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S03116; S03116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                            Local Similarity
Les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                          NCBI_TaxID-10116;
1176
1309
1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M23572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
TYRO_RANNI
ID TYRO_RANNI
                                                                                                                                                                                                                                                                                                                                                                                                                                 INSULIN
 CARBOHYD
          CARBOHYD
                              SEQUENCE
                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                               G33_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                           RESULT 13
                                                                                                                                                      G33_RAT
 EEES
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                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. : .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOPAQUINONE + H(2)O.
-! COFACTOR: BINDS TWO COPPER IONS.
-! SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
-! SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
                                                                                                                                                                                                              MEDILINE-93077054; PubMed-1446833; Takese M., Miura I., Nakata A., Takeuchi T., Nishioka M.; Takase M., Miura I., Nakata A., Takeuchi T., Nishioka M.; Toloning and sequencing of the cDNA encoding tyrosinase of the Japanese pond frog, Rana nigromaculata."; Gene 121:359-363(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUMENAL, MELANOSOME (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COPPER A (BY SIMILARITY).
COPPER A (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B27D3080F0C74B3A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. . .)
(GLCNAC. . .)
(GLCNAC. . .)
                                                                                     Rana nigromaculata (Japanese pond frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50.5; 1
Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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N-LINKED
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N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JC1392; JC1392.
InterPro; IPR00227; Tyrosinase.
Pfam; PF00264; tyrosinase; 1.
PRNTYS; PR009092; TYROSINASE.
PROSITE; PS00497; TYROSINASE.
PROSITE; PS00499; TYROSINASE.
                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Blood;
MEDLINE-95290234; PubMed-7772385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60115 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D12514; BAA02077.1; -. EMBL; D37779; BAA07034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.1%;
                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE OF 1-277 FROM N.A.
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                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=8409;
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                      Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
    13;
                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 322;
   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                 4 CRFG----TCTVQK--LAHQIYQFTDKDKD-----NVAPRSKISP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .EMBL; AE000081; AAB91733.1; -. Hypothetical protein; Plasmid. SEQUENCE 322 AA; 36690 MW; 177BOAF61FA0C74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                           Y4KA_RHISN STANDARD; PRT; 322 AA. P55521; 01.NOV-1997 (Rel. 35, Created) 01.NOV-1997 (Rel. 35, Last sequence update) 01.NOV-1997 (Rel. 35, Last annotation update) Hypothetical 36.7 kDa protein Y4KA.
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.6%; Score 49.5; [35.3%; Pred. No. 17; tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=97305956; PubMed=9163424;
   8;
                                                                                                                                                                                                                                                       Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
   Conservative
                                                                                                                                                                                                                                                                                                       Rhizobiaceae; Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=394;
16;
                                                                                                                             Y4KA_RHISN
 Matches
                                                                                                            RESULT 15
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210 GQPKVNKLADEI-QFTTKNSFSATPSAELDPANH 242

oy da Search completed: October 17, 2002, 14:49:12 Job time : 4.39401 secs

7 GTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40

1 3

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

October 17, 2002, 14:45:20 ; Search time 4.58853 Seconds (without alignments) 837.648 Million cell updates/sec

US-10-018-924-2_COPY_107_146
219
1 SFGCRFGTCTVQKLAHQIXQFTDKDKDNVAPRSKISPQGY 40 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	adrendedili		adrenomedullin pre	•	ar multi	multidrug resistan	ga]	hypothetical prote	S-locus-specific q		lipopolysacharide	S-100us-specific	-locus-spec	10018-80001-	S-locus-specific a	hypothetical prote	-10018-8080	S-locus-specific a	S-recentor kinase	-locus-specific	S-locus-specific a	vpothetical prot		hypothetical prote	S-locus-specific a	ARC transporter AT			hypothetical prote	
SUMMARIES	ID	JN0684	S41600	JN0766	T14536	S71839	S71841	A99638	A85489	T14415	T14529	G84107	T07814	A27827	T14424	T14423	T15540	T14416	T14530	T07809	T07810	T14528	E91004	E85637	. 520799	T14533	AD2000	T16368	T14471	083	
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	Length	185	188	185	430	1541	1545	189	189	431	428	373	428	436	427	428	465	428	428	429	426	429	93	93	319	429	608	759	857	171	
dР	Query Match	100.0	97.3	89.5	28.1	27.9	26.9	26.7	26.7	26.7	25.3	25.1	24.9	24.9	24.4	24.4	24.2	24.0	24.0	24.0	23.5	23.5	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.1	
	Score	219	213	196	61.5	61		58.5					54.5				53	52.5	52.5	52.5	51.5	51.5	51	51	51	51	51	51		50.5	
	Result No.	1	7	m	4	'n	9	7	ω.	σ,	10	11	12	13	14	15	16	. 17	18	19	20	21	22	23	24	25	56	27	28	29	

hypothetical prote	monophenol monopay	hypothetical prote	S-receptor kinase	S-receptor kinase	hypothetical profe	mvb-related transc	hypothetical prote	exonuclease Shor	hypothetical profe	hypothetical prote	hypothetical prote	Conserved hypothet	Sugar phosphate nu	S-locus-specific 9
T27938 S03116	JC1392	S58319	T14472	JQ1677	C86279	T51674	T05996	AB0551	T47067	T48354	C97389	AD2607	F90507	T07812
9,0	7	7	~	Н	~	~	~	7	7	~	~	7	~	7
419	532	587	850	828	90	171	250	1034	322	356	204	204	253	431
23.1	23.1	23.1	23.1	23.1	22.8	22.8	22.8	22.8	22.6	22.6	22.4	22.4	22.4	22.4
50.5	50.5	50.5	50.5	50.5	20	20	20	20	49.5	49.5	49	49	49	49
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

JN0684 adrenomedullin precursor - human C.Species: Homo saniens (man)
R.Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto, Blochem. Blophys. Res. Commun. 203, 631-639, 1994
A.Title: Genomic structure of human adrenomedullin gene. A.Reference number: JC2351: MITD: 9434486
A, Accession: JC2351
A;Wolecule type: DNA A;Residues: 1-185 <ish></ish>
A;Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
n. A.Pollinium, and John C. M. Millory Louine, M. M. Matsuo, H.: Eto, T. R. Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.: Eto, T.
Blochem. Biophys. Res. Commun. 194, 720-725, 1993.
A) Reference number: JN0684; MUID:93343928
A; Accession: JN0684
A:MOLECULE Cype: MRNA A:Residines: 1-185
A; Cross-references: GB: D14874; NID: 9455470; PIDN: BAA03589.1; PID: 9500612
A; Accession: PN0548
A.Molecule type: protein
Any incompanies of at Antick Refigning K ventures K ventures W ventures M ven
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A; Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A; Reference number: JN0476; MUID:93249425
A; Accession: JN0476
A; Molecule type: protein
A; Residues: 95-146 < KI3>
Ajexperimental source: pneocnromocytoma
A.Gene: GDB: ADM
A;Cross-references: GDB:217070; OMIM:103275
A.Map position: 11pter-11qter
A; Introns: 33/2; 83/2
C: Keywords: amidated carboxyl end; blood pressure control; hormone
F:/I-ZJUONAIN: Signal sequence #Status predicted <sig> F:22-185/Product: proadresomedullis #status predicted <sig></sig></sig>
F;22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <pap></pap>
F;95-146/Product: adrenomedullin #status experimental <mat></mat>
Fild7-185/Domain: carboxyl-terminal propeptide *status predicted <ctp></ctp>
Fig. 115/Displfide honds: #status experimental
F:146/Modified site: amidated carboxyl end (TVI) (amide in mature form from following
North () +

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Gaps

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Query Match 100.0%; Score 219; DB 2; Length 185; Best Local Similarity 100.0%; Pred. No. 8.8e-23; Matches 40; Conservative 0; Mismatches 0; Indels

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S71839
canalicular multidrug resistance protein - rat
C;Species; Rattus norvegicus (Norway rat)
C;Species; Rattus norvegicus (Norway rat)
C;Species; Rattus norvegicus (Norway rat)
C;Accession: 571839
R;Ruechler, M; Koenig, J; Brom, M; Kartenbeck, J; Spring, H; Horie, T; Keppler,
T; Ruechler, M; Koenig, J; Brom, M; Kartenbeck, J; Spring, H; Horie, T; Keppler,
J; Biol. Chem, 271, 15091-15098, 1996
A;Title: cDNA cloning of the hepatcoyte canalicular isoform of the multidrug resistan
A;Residue: preliminary, nucleic acid sequence not shown
A;Residue: preliminary, nucleic acid sequence not shown
A;Residue: preliminary, nucleic acid sequence not shown
A;Residue: 171839
A;Resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons
                                                                                                                                                                                                                                 A, Accession: T14536
A, Status: preliminary: translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-430 < KUS>
A, Cross-references: EMBL:D85212; NID:q2351155; PIDN:BAA21946.1; PID:q2351156
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multidrug resistance protein, canalicular - human
C;Species: Homo saplens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: S71841; S71840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61.5; DB 2;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               canalicular - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
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                                                                                                                                                                                        A; Reference number: Z18078; MUID: 97352858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.6%;
Matches 14; Conservative 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                        echanism.
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A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control.
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, J.; Shim
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E;1-21/Domain: signal sequence #status predicted <SIG>
E;1-21/Domain: signal sequence #status predicted <PBU>
E;22-11/Product: proadrenomedullin #status predicted <PAT>
E;94-14/3/Product: adrenomedullin #status predicted <WAT>
E;94-14/3/Product: adrenomedullin #status predicted <WAT>
E;1/Modified site: amidated carboxyl end (Aray) (amide in mature form from following 9:
F;14/3/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following 9:
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C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Complete amino acid sequence of porcine adrenomedullin and cloning A; Reference number: $41600; MUID:94139945 A; Accession: $41600
                                                                                                                                                                                                                                                                                                                                                                       direntomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Becies: Sus scrofa domestica (domestic pig)
C;Becession: S41600
R;Kitemura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
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A;Molecule types: mRNA
Residues: 1-188 <KITT>
A;Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379
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Pred. No. 1.4e-19;
Trefines 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                              SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
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Pred. No. 6.1e-22;
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1 Similarity 87.5%;
35; Conservative
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Best Local Similarity 97.5%;
Matches 39; Conservative
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A; Residues: 1-185 <SAK>
A; Accession: PN0610
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Best Local 3
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Matches
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A'Accession: A85489
A'Status: preliminary
A'Status: preliminary
A'Molecule type: DNA
A'Residues: 1-189 CATO>
A'Cross-references: GB:AE005174; NID:g12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP:
A'Cross-references: strain 0157:H7, substrain EDL933
C'Genetics:
A'Gene: Z0078
C'Superfamily: Escherichia coli yabp protein
                      iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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N.Alternate names: S glycoprotein
C.Specias: Brassica oleracea (wild cabbage)
C.Specias: Brassica oleracea (wild cabbage)
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C.Accession: T14529
R.Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A.Title: Striking sequence similarity in inter- and intra-specific comparisons of clechanism.
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A;Molecule type: DNA
A;Molecule type: DNA
A;Ecsidues: 1.431 «KUS>
A;Cross-references: EMBL:DB5215; NID:g2351161; PIDN:BAA21949.1; PID:g2351162
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
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A;Cross.references: EMBL:D85205; NID:g2351141; PIDN:BAA21939.1; PID:g2351142
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
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R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons
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C'Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
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26.7%; Score 58.5; DB 2; Length 431;
Best Local Similarity 32.7%; Pred. No. 3.7;
Matches 16; Conservative 8; Mismatches 14; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 GVRFSGMPGDQKLNYMYYNFTENSEDVAYTFRMTNKSIYSRLKISSEGF 270
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                                                                                                                                                                                                                                                                                                                                                                                                          DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Mismatches
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95 KLTHWLIKFNELKEYAKDPENMAARASLSPEG 126
                                                                                                                                                                                                                                                                                                                                                                                                     Score 58.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 KLAHQIYQFTD----KDKDNVAPRSKISPQG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                echanism.
A;Reference number: 218078; MUID:97352858
A;Accession: T14415
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A; Accession: T14529
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Best Local Similarity 34.4%;
Matches 11; Conservative
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                                                                           RESULT 8
A85489
APOCHACICAL PROTECT 20078 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Accession: A85489
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ECs0073 [imported] - Escherichia coli (strain O157:H7, substrain RI C.Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Barbarichia coli (Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Accession: A99638 R; Haysahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. DNA Res. 8, 11-22, 2001 A; Filtle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gency Ascession: A99638 A; Status: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:ABCC2; CMOAT; ABC; MRP2; CMRP; DJS
A;Cross-references: CDB:6089489; OMIM:601107
A;Map position: 10q24-10q24
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology C,Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology C,Superfamily: ATP-binding cassette homology CABC1>
F;654-837/Domain: ATP-binding motif A (P-loop)
F;5117-1510/Domain: ATP-binding cassette homology CABC2>
F;1317-1510/Domain: ATP-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 26.9%; Score 59; DB 1
1 Similarity 37.8%; Pred. No. 12;
14; Conservative 5; Mismatches
R;Koenig, J.; Keppler, D. submitted to the EMBL Data Library, August 1996 A;Reference number: S71841 A;Accession: S71841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58.5; D
Pred. No. 1.6;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 KLAHQIYQFTD----KDKDNVAPRSKISPQG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: ECs0073
C;Superfamily: Escherichia coli yabP protein
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Best Local Similarity 34.4%;
Matches 11; Conservative
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Matches 14; Conserv
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 $^{\rm cl}$

Length 428;

DB 2;

Score 55.5;

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S-locus-specific glycoprotein - turnip (fragment)
N.Alternate names: S glycoprotein
N.Alternate names: S glycoprotein
C; Species: Brasslca rapa (turnip)
C; Species: Brasslca rapa (turnip)
C; Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C; Accession: T14423
R; Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-768, 1997
A; Title: Striking sequence similarity in inter- and intra-specific comparisons of clechanism.
A; Reference number: 218078; MUID:97352858
A; Accession: T14423
A; Accession: T14423
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-428 <KUS>
A; Residues: EMBL: D85223; NID: 92351177; PIDN: BAA21957.1; PID: 92351178
A; Cross-references: EMBL: D85223; NID: 92351177; PIDN: BAA21957.1; PID: 92351178
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D85225; NID:92351181; PIDN:BAA21959.1; PID:92351182
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
     A;Title: Amino-acid sequence of glycoproteins encoded by three alleles of the S locus A;Title: Amino-acid sequence of glycoproteins encoded by three alleles of the S locus A;Reference number: A93392
A;Reference number: A93392
A;Reference number: A1827
A;Reference number: A1827
A;Residues: 1-436 < NAS>
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology C;Reywords: glycoprotein
F;32-436/Porduct: S-locus-specific glycoprotein S6 #status predicted <MAT>
F;32-436/Pomain: S-locus-specific glycoprotein homology <SSG>
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N;Alternate names: S glycoprotein
C;Specias: Brassica rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14424
R;Kusaba, M; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
R;Kusaba, M; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 GVRFSGIPEDQKLSYMVXNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GCRF-GICIVOKLAHQIYQFTDKDKD------NVAPRSKISPQGY 40
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24.4%; Score 53.5; DB 2;
Best Local Similarity 28.6%; Pred. No. 18;
Matches 14; Conservative 10; Mismatches 14;
                                                                                                                                                                                                                                                                                                                       DB 2;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-427 < KUS>
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28.6%; Pred. No. 18;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                    24.9%; Score 54.5; D 28.6%; Pred. No. 13; ive 10; Mismatches
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Best Local Similarity 28.6%
Matches 14; Conservative
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Best Local Similarity 28.69
Matches 14; Conservative
Nature 326, 617-619, 1987
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T14424
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C;Species: Raphanus sativus (radish)
C;Species: Raphanus sativus (radish)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07814
R;Sakamorto, K:; Kusaba, M:; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A;Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related gen A;Reference number: 216146; MUID:98311079
                                                                                                                                                                                                                                                                                                                  C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
R;Accession: 084107
R;Takami, H: Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-373 <STO>
A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07382.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                            C-125)
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                                                                                                                                                                                                                                                                               lipopolysaccharide biosynthesis BH3663 [imported] - Bacillus halodurans (strain
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A; Residues: 1-428 <SAK>
A; Cross-references: EMBL:AB009682; NID:g3327849; PIDN:BAA31729.1; PID:g3327850
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S-locus-specific glycoprotein S6 precursor - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 15-Nov-1996
C;Accession: A27827
R;Nasrallah, J.B.; Kao, T.H.; Chen, C.H.; Goldberg, M.L.; Nasrallah, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                             219 GVRFSGIPENOKLSYMVINFTENSEEVAYTFRMINNSFYSRLKVSSDGY 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 373;
                                                                                           ---NVAPRSKISPQGY 40
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                                        Indels
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Pred. No. 13;
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                                        Mismatches
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9
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                    Pred.
                                                                                              GCRF-GTCTVQKLAHQIYQFTDKDKD---
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30.6%;
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              30.6%;
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                                                Conservative
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Les 15; Conserv
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Best Local Similarity
Matches 13; Conserv
                    Similarity
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A;Gene: SLG(S6)
                                                   15;
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Novel human diagno Novel human diagno Kojibiose phosphor Novel human diagno Novel human diagno Orosophila melanog

OM protein

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Sequence: Perfect

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Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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                                                                                                                                           AAB91765
AAW25160
AAB91762
AAE09827
AAW33361
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AAB91767
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   10-OCT-2000; 2000WO-JP07023.
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N-PSDB; AAH19806.
WO200127310-A1.
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Glycine extended a
Linker peptide-adr
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UspA(1-66) (DD) (G
UspA(1-49) (A) (GS
Thioredoxin (GSGSG
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                                                                                                October 17, 2002, 14:45:20; Search time 9.67581 Seconds (without alignments) 459.181 Million cell updates/sec
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1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
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Copyright (c) 1993 - 2002 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                       producing the fused
                                   adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaccutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                               Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                   Length 52;
                             producing
                                                                                                                                                                                                             Indels
                             present invention describes a method (M1) for
                                                                                                                                                                                   Score 219; DB 22;
Pred. No. 2.5e-24;
                                                                                                                                                                                                                                     SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
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                                                                                                                                                                                                                                                  Query Match 100.0%; Score 219; I Best Local Similarity 100.0%; Pred. No. 2.5 Matches 40; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Adrenomedullin peptide (AM) SEQ ID NO:935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 498; 733pp; English.
  Page 45; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Milner PG,
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                               AAB91759 standard; Peptide;
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                                                                                                                                                            52 AA;
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10-SEP-1999;
15-OCT-1999;
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        Disclosure;
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Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vasoactive peptides useful for inhibiting calcitonin gene related
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Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 40; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                      Score 219; DB 22;
Pred. No. 2.5e-24;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Column 25-26; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A'A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adrenomedullin peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE09818 standard; peptide; 52
                                                                                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saha S, Abel PW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide receptor activity
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adrenomedullin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCR-) UNIV CREIGHTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-564216/63
                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                              52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-1998;
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AAB75111;

AAB7511 RESULT

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for pharmaceutical and diagnostic fused adrenomedullin precursor using a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linker peptide-adrenomedullin (AM) precursor protein.
                                                                                                                                                                                                 Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 219; DB 22;
Pred. No. 2.6e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
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100.0%; Pred. No. 2..
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 47; 75pp; Japanese.
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                                                                                                                                                                                                                                                                                                          application comprises producing recombinant host
                                                                                                                                                                                                                                                                                        Producing adrenomedullin useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB75113 standard; Protein; 62
                                                                                                                          99JP-0294147
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                                                                                                                                                            SHIO ) SHIONOGI & CO LTD
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N-PSDB; AAH19809.
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Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 AA;
                                                                                                                                                                                                                                                        N-PSDB; AAH19808
             WO200127310-A1.
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                                                                                      10-OCT-2000;
                                                                                                                          15-0CT-1999;
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                                                                                                                                                                                               Takimoto A,
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                                                   19-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                                                                                                   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                             Glycine extended human adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine extended adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 219; DB 22; ilarity 100.0%; Pred. No. 2.6e-24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 46; 75pp; Japanese.
                                        AAB75111 standard; Protein; 53 AA.
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                                                                                                                                                                                                                                                                                                                                                    10-OCT-2000; 2000WO-JP07023.
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                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-282044/29.
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Best Local Similarity
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                                                                                                                                                                                                                                                                           WO200127310-A1
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                                                                                                              31-JUL-2001
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Synthetic.
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RESULT 5

AAB75112;

Sequence

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Gaps

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Length 53; Indels exemplification of the present invention

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The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a
                                                                                                                                adrefrommedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adrenomedullin, glycine extended adrenomedullin, AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 rrouncing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host
                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                  The present invention describes a method (M1) for producing
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                                                                                                                                                                                                                                                                                                                         Score 219; DB 22;
Pred. No. 3.1e-24;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                             SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                              SPGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 68; 75pp; Japanese.
                                                                                    75pp; Japanese.
                                                                                                                                                                                                                                                                                                                          100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB75122 standard; Protein; 120
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                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-282044/29
                                                                                    Page 48;
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                          62 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant host
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Best Local Simi
Matches 40;
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                                                                                    Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB75122;
                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
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                                                                                                                                                                                                                                                                                            Adrenomedullin; glycine extended adrenomedullin; AM: AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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100.0%; Pred. No. 6.6e-24;
iive 0; Mismatches 0;
                                                                                                                80 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 119
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                                                            6.6e-24;
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                                                DB
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                                                                          Mismatches
                                              Score 219;
Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 69-70; 75pp; Japanese.
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                                                 100.0%;
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                                                                                                                                                                                                                                            (first entry)
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                                                              Local Similarity
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                        120 AA;
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N-PSDB; AAH19865
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                    AAB75123;
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                          Seguence
                                                 Query Match
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                                                                            Matches
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Gaps

RESULT 9

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adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                          Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Passive elongation; vesicle smooth muscle; uropathic activity;
                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adrenomedulin; urinary disorder; incontinence; human
                                                                                                                                                                                    Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 219; DB 22;
ilarity 100.0%; Pred. No. 9.8e-24;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adrenomedulin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 49-50; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB49697 standard; Protein; 185
                                                                  10-OCT-2000; 2000WO-JP07023.
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                                                                                                                                                                                  Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises adrenomedulin
                                                                                                                                           OS SHIONOGI & CO
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N-PSDB; AAF29138.
                                                                                                                                                                                                                     2001-282044/29
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 AA;
                                                                                                                                                                                                                                       N-PSDB; AAH19810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200078338-A1
                                                                                                       15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                              Takimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-1999;
                               19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB49697;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
                                                                                                                                                 Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; glycine extended adrenomedullin; AM; AM-gly;
precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 22;
. 8.3e-24;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               th 100.0%; Score 219; D
Similarity 100.0%; Pred. No. 8.3
40; Conservative 0; Mismatches
                                                                                                          UspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thioredoxin-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takimoto A, Mitsuda Y, Nakayama T,
AAB75124 standard; Protein; 147 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 71; 75pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                      10-OCT-2000; 2000WO-JP07023
                                                                                                                                                                                                                                                                                                                                                                             99JP-0294147
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                (SHIO ) SHIONOGI & CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AA;
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                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1999;
                                                                         31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
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                                                                                                                                                                                                                           Synthetic.
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Sequence Query Match

Local Best Loca Matches AAB75114;

RESULT 10

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Synthetic

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Length 170;

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Gaps

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Mismatches

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Conservative

40;

Matches

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                                      This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the human adrenomedulin protein, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorthoea. The present sequence represents human adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                   Length 185;
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                                                                                                                                                                                                                    ; DB 22;
1.1e-23;
                                                                                                                                                                                                                                                                                                   Score 219; DB 22;
Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                 1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                    100.0%; Score 219;
                                                                                                                                                                                                                                       Pred. No.
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           Claim 1; Page 26-27; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                 AAB60344 standard; Protein; 185
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0
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                                                                                                                                                        the invention.
                                                                                                                                                                                                                                     100.0%;
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21-MAR-2000; 2000JP-0079171.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 37-38;
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                                                                                                                                                                                                                                  Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                      composition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB60344;
                                                                                                                                                                                        Sequence
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Length 185;

100.0%; 100.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;
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                                                                                                                                                                                                                        Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; procine.
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                    107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
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Pred. No. 8.2e-23;
0; Mismatches 1;
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1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                               Porcine adrenomedulin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 31-33; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB60345 standard; Protein; 188 AA
                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine adrenomedullin precursor.
                                                                                                         AAB49698 standard; Protein; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.3%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                             23-JUN-2000; 2000WO-JP04166.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises adrenomedulin
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N-PSDB; AAF29139.
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Best Local Similarity
Matches 39; Conserv
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                                                                                                                                                                                                                                                                                                    WO200078338-A1.
                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1999;
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                                                                                                                                                                                                                                                                        Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                              RESULT 13
                                                                                         AAB49698
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1 STGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 40
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       (CONJ-) CONJUCHEM INC.
                           Bridon DP,
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                                                                                                                                                                                                                                                                                            The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmeorthoea. The present sequence represents porcine adrenomedullin precursor.
                                                                                                                                                                                                                                     Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
uterine contraction inhibitor; premature birth; miscarriage; abortion; dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 213; DB 22;
Pred. No. 8.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adrenomedullin peptide (AM) SEQ ID NO:944.
                                                                                                                                                                                                                                                                         Disclosure; Page 43-44; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB91768 standard; Peptide; 40 AA
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99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                         97.3%;
97.5%;
                                                                                                                           23-JUN-1999; 99JP-0177548,
21-MAR-2000; 2000JP-0079171,
                                                                                                    23-JUN-2000; 2000WO-JP04167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-2001 (first entry)
                                                                                                                                                           (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Conservative
                                                                                                                                                                                                      WPI; 2001-080755/09
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   188 AA;
                                                                                                                                                                                                                   N-PSDB; AAF27229
                                                       WO200078339-A1
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10-SEP-1999;
15-OCT-1999;
                                                                                                                          23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Synthetic.
                                                                              28-DEC-2000
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                                                                                                                                                                                 Yanagita T;
                                  Sus scrofa,
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB91768;
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a

reactive group (II) (e.g. succinimidyl and malelmido groups) attached to

a less therapeutically active amino acid region (IV), which covalently

bonds with amino/pydroxyl/thiol groups on blood components to form a

peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth

in vivo for the treatment of various disorders. Endogenous therapeutic

peptides are not suitable as drug candidates as they require frequent

administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or

reduces the action of peptidases to increase length of activity (half

info and specificity as bonding to large molecules decreases

and specificity as bonding to large molecules decreases

ABB90829 to AAB92441 represent invention.
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                                                                                                                                  Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
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   Thibaudeau K;
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   Holmes DL,
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llarity 87.5%; Pred. No. 4e-21;
Conservative 3; Mismatches
                                                                                                                                                                                                                                                                            Disclosure; Page 502; 733pp; English.
Milner PG,
Ezrin AM,
                                                               WPI; 2001-112059/12
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Best Local Similarity
Matches 35; Conserv
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